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OM protein - protein search, using sw model

Run on: November 13, 2003, 14:59:16 ; Search time 40 Seconds

(Without alignments)  
841.251 Million cell updates/sec

Title: US-09-902-705-2

Perfect score: 1116

Sequence: 1 MATSPGVWIMDDWPGYDLN.....LDYNEYPDLNHICVINEHG 212

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 19Jun03.\*

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23: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1116	100.0	212	17 AAR98224	Hypoxanthine guani
2	1069	95.8	225	21 AAY79212	Human transferase
3	1065	95.4	225	22 AAB94995	Human protein sequ
4	1065	95.4	230	23 ABP41467	Human ovarian anti
5	772	69.2	218	18 AAW37339	Mouse HPRT.
6	445.5	39.9	231	22 AAB85165	P. falciparum HGPR
7	265.5	23.8	180	23 ABB54862	Lactococcus lactis
8	261	23.4	183	23 ABB53319	Lactococcus lactis
9	257.5	23.1	180	23 ABP27993	Streptococcus poly

10	251.5	22.5	194	22 AAG92711	C glutamicum prote
11	251.5	22.5	200	22 AAB80144	Corynebacterium gi
12	250.5	22.4	648	23 ABB47663	Listeria monocytog
13	247.5	22.2	180	19 AAW80653	S. pneumoniae puta
14	247.5	22.2	180	24 ABU02782	S. pneumoniae type
15	245.5	22.0	180	22 AAM01114	CPE 117 protein se
16	243	21.8	58	21 AAG02773	Human secreted pro
17	238.5	21.4	181	23 ABP38473	Staphylococcus epi
18	232.5	20.8	180	23 ABP27992	Streptococcus poly
19	225.5	20.2	187	22 AAU41731	Propionibacterium
20	209.5	18.8	188	21 AAG21927	Arabidopsis thalia
21	209.5	18.8	188	23 ABB91553	Herbicidally activ
22	209.5	18.8	193	21 AAG21926	Arabidopsis thalia
23	208.5	18.7	187	23 ABP66271	Blifidobacterium lo
24	147	13.2	56	21 AAB59068	Breast and ovarian
25	143	12.8	127	23 ABP35009	Human transferase
26	138.5	12.4	200	24 ABP77089	N. gonorrhoeae ami
27	122.5	11.0	173	24 ABU01712	S. pneumoniae type
28	117	10.5	192	22 AAG91529	C glutamicum prote
29	114.5	10.3	173	23 ABP26684	Streptococcus poly
30	113.5	10.2	194	22 AAU51709	Propionibacterium
31	110	9.9	173	23 ABB54950	Lactococcus lactis
32	108.5	9.7	173	23 ABP30396	Streptococcus poly
33	108.5	9.7	185	23 ABP26683	Streptococcus poly
34	103.5	9.3	155	22 AAB96065	Puative P. abyss
35	96	8.6	182	20 AAY06888	S. aureus pyrk hom
36	94	8.4	440	22 ABG15272	Novel human diagno
37	94	8.4	573	22 ABG28703	Novel human diagno
38	91.5	8.2	183	23 ABB47706	Listeria monocytog
39	89	8.0	187	23 ABP39935	Staphylococcus epi
40	88.5	7.9	199	21 AAY74558	Neisseria gonorrhe
41	88.5	7.9	199	21 AAY74560	Neisseria meningit
42	88.5	7.9	199	24 ABP81041	N. gonorrhoeae ami
43	87.5	7.8	199	21 AAY74559	Neisseria meningit
44	87	7.8	494	19 AAW69250	Human p56-2 protei
45	87	7.8	494	21 AAY78948	Human p56-2 amino

#### ALIGNMENTS

#### RESULT 1

AAR98224

ID AAR98224 standard; Protein; 212 AA.

AC AAR98224;

DT 24-SEP-1996 (first entry)

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PT DNA encoding human hypoxanthine guanine phosphoribosyl transferase  
PT 2 - provides a polypeptide capable of therapeutic end use in purine  
PT synthesis disorders  
XX  
PS Claim 14; Page 33-34; 50pp; English.  
XX  
CC Human hypoxanthine (guanine) phosphoribosyl transferase 2 (HPRT-2)  
CC (AA898224) is utilised by mammalian cells for the salvage of purines,  
CC preventing the formation of uric acid. Its amino acid sequence  
CC was deduced from a cDNA clone (AA830127) isolated from a foetal  
CC lung library. Recombinant HPRT-2 can be expressed in prokaryotic  
CC or eukaryotic (e.g. COS, Sf9) host cells. It can be used to  
CC prevent or treat Lesch-Nyhan syndrome, kidney stones, renal  
XX failure, uricaciduria, precocious gout, anaemia and  
CC nephrolithiasis. It is also used to screen for HPRT-2  
CC antagonists and to raise antibodies.  
XX  
SQ Sequence 212 AA;  
Query Match 100.0%; Score 1116; DB 17; Length 212;  
Best Local Similarity 100.0%; Pred. No. 1.9e-115;  
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MATSPGVIMDDPGYDLNLFTYPOHYVYGDLEVLIPHGIIIVDRIERLAKDIMKDIGYS 60  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Dy 1 MATSPGVIMDDPGYDLNLFTYPOHYVYGDLEVLIPHGIIIVDRIERLAKDIMKDIGYS 60  
QY 61 DIMVLVLKGGYKFCADLVEHLKNTSRNSDRFVSMKVDFIRLKSYNDSQMGEMOTIIGG 120  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Dy 61 DIMVLVLKGGYKFCADLVEHLKNTSRNSDRFVSMKVDFIRLKSYNDSQMGEMOTIIGG 120  
QY 121 DLSTLAKNFLIVEDVVGTRTKMALLSNIEKYKPNMIVASLLVKRTSRSDGFRPDYAG 180  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Dy 121 DLSTLAKNFLIVEDVVGTRTKMALLSNIEKYKPNMIVASLLVKRTSRSDGFRPDYAG 180  
QY 181 FEIPLFVVGVALDYNEFRDLNHCIVINEHG 212  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Dy 181 FEIPLFVVGVALDYNEFRDLNHCIVINEHG 212  
RESULT 2  
ID AAY79212 standard; Protein; 225 AA.  
XX  
AC AAY79212;  
XX  
DT 19-JUN-2000 (first entry)  
XX  
DE Human transferase TRNSFS-4.  
XX  
KW Transferase; TRNSFS-4; human; antitumour; cancer;  
KW gastrointestinal disorder; developmental disorder;  
KW genetic disorder; neurological disorder; reproductive disorder;  
KW smooth muscle disorder; immunological disorder; inflammation;  
KW diagnosis; hypoxanthine (guanosine) phosphoribosyltransferase;  
KW therapy.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 176  
FT Modified-site 4 /note= "potential O-phosphorylation"  
FT Modified-site 117  
FT Modified-site 155 /note= "potential O-phosphorylation"  
FT Modified-site 96 /note= "potential O-phosphorylation"  
FT Modified-site 101 /note= "potential O-phosphorylation"  
FT Modified-site 111 /note= "potential O-phosphorylation"

FT Modified-site /note= "potential O-phosphorylation"  
FT 146  
FT Modified-site /note= "potential O-phosphorylation"  
FT 149  
FT Modified-site /note= "potential O-phosphorylation"  
FT 175  
FT Modified-site /note= "potential O-phosphorylation"  
FT 91  
FT Modified-site /note= "potential N-glycosylation"  
FT 35..225  
FT Domain /note= "purine/pyrimidine  
phosphoribosyltransferase domain"  
XX  
PN WO200014251-A2.  
XX  
PD 16-MAR-2000.  
XX  
PF 09-SEP-1999; 99WO-US20989.  
XX  
PR 10-SEP-1998; 98US-0150657.  
PR 04-NOV-1998; 98US-0186779.  
PR 11-MAY-1999; 99US-0133642.  
XX  
XX (INCY-) INCYTE PHARM INC.  
PA  
XX Tang YT, Corley NC, Guegler KJ, Baughn MR, Lal P, Yue H;  
PI Hillman JL, Azimzai Y;  
DR WPI: 2000-256996/22.  
DR N-PSDB; AA294204.  
XX  
PT Human transferase proteins useful for preventing, diagnosing and  
PT treating cancers and developmental, gastrointestinal, genetic,  
PT immunological, neurological, reproductive and smooth muscle disorders -  
XX  
PS Claim 1; Page 82-83; 113pp; English.  
XX  
XX The present sequence is that of human transferase TRNSFS-4, 1 of  
CC 15 claimed novel human transferase proteins of the invention (see  
CC AA79209-23). The sequence was deduced from a cDNA clone (see  
CC AA294204) isolated from a myxoma tissue library. It shows homology  
CC to hypoxanthine (guanine) phosphoribosyltransferase. TRNSFS-4 is  
CC expressed in nervous, cardiovascular, gastrointestinal,  
CC reproductive, haematopoietic and nervous tissues, especially those  
CC associated with cancer and inflammation. The new human transferase  
CC proteins and the polynucleotides encoding them can be used in the  
CC diagnosis, prevention and treatment of cancer, developmental  
CC disorders, gastrointestinal disorders, genetic disorders,  
CC immunological disorders, neurological disorders, reproductive  
CC disorders, and smooth muscle disorders. The polypeptides can also  
CC be used to raise antibodies, and to screen for agonists and  
CC antagonists of transferase activity.  
XX  
SQ Sequence 225 AA;  
Query Match 95.8%; Score 1069; DB 21; Length 225;  
Best Local Similarity 98.5%; Pred. No. 3.4e-110;  
Matches 203; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 7 GVIMDDPGYDLNLFTYPOHYVYGDLEVLIPHGIIIVDRIERLAKDIMKDIGYSIMVLC 66  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Dy 14 GVIMDDPGYDLNLFTYPOHYVYGDLEVLIPHGIIIVDRIERLAKDIMKDIGYSIMVLC 73  
QY 67 VLKGGYKFCADLVEHLKNTSRNSDRFVSMKVDFIRLKSYNDSQMGEMOTIIGGDLSTLA 126  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Dy 74 VLKGGYKFCADLVEHLKNTSRNSDRFVSMKVDFIRLKSYNDSQMGEMOTIIGGDLSTLA 133  
QY 127 GKNFLIVEDVVGTRTKMALLSNIEKYKPNMIVASLLVKRTSRSDGFRPDYAGFEIPLH 186  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Dy 134 GKNFLIVEDVVGTRTKMALLSNIEKYKPNMIVASLLVKRTSRSDGFRPDYAGFEIPLH 193  
QY 187 FVVGVALDYNEFRDLNHCIVINEHG 212  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||



disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and vaginitis), immune disorders (e.g., congenital and acquired immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), blood-related disorders (e.g., anaemia), cardiovascular disorders, respiratory disorders, neurological disorders, gastrointestinal disorders and urinary system disorders. Ovarian antigen polypeptides and polynucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may further be used for gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents a human ovarian antigen of the invention. CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 230 AA;  
 Query Match 95.4%; Score 1065; DB 23; Length 230;  
 Best Local Similarity 98.5%; Pred. No. 9.7e-110;  
 Matches 203; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 GVVIMDDPGYDLNFTYPQHYGGDLEVLPHGIIIVDRIERIAKDIMKDIGSDIMVLC 66  
 DB 19 GVVIMDDPGYDLNFTYPQHYGGDLEVLPHGIIIVDRIERIAKDIMKDIGSDIMVLC 78  
 QY 67 VLKGGYKFCADLVEHLKNI SRNSDRFVSMKVD FIRLKS YRNDQSGMGEMQIIIGGDLSTL 126  
 DB 79 VLKGGYKFCADLVEHLKNI SRNSDRFVSMKVD FIRLKS YRNDQSGMGEMQIIIGGDLSTL 138  
 QY 127 GKNFLIVDVGTGRMTKALLNIEKYKPNMIVKASLLVKRTSRSDGFRPDYAGFEIPL 186  
 DB 139 GRNVLIVDVGTGRMTKALLNIEKYKPNMIVKASLLVKRTSRSDGFRPDYAGFEIPL 198  
 QY 187 FVVGVALDYNEFRDLNHCIVNEHG 212  
 DB 199 FVVGVALDYNEFRDLNHCIVNEHG 224

RESULT 5  
 AAW37339  
 ID AAW37339 standard; Protein; 218 AA.  
 XX AAW37339;  
 AC AAW37339;  
 DT 11-MAY-1998 (first entry)  
 XX Mouse HPRT.  
 DE  
 KW Vaccine, B-cell malignancy; lymphoma; leukaemia; tumour;  
 KW gene amplification; immunotherapy; therapy; mouse; HPRT;  
 KW hypoxanthine-phosphoribosyltransferase; selectable marker;  
 KW vector; pMSD5-HPRT.  
 OS Mus musculus.  
 XX WO9741244-A1.  
 EN  
 PD 06-NOV-1997.  
 XX  
 PF 25-APR-1997; 97WO-US07039.  
 XX  
 PR 06-DEC-1996; 96US-0761277.  
 PR 01-MAY-1996; 96US-0644664.  
 XX  
 PA (GENI-) GENITOPE CORP.  
 XX  
 PI Denney DW;  
 XX  
 DR WPI; 1997-549743/50.  
 DR N-PSDB; AAT97166.

XX Multivalent vaccine to treat B cell lymphoma or leukaemia -  
 PT comprises at least 2 different recombinant variable regions of  
 PT immunoglobulin molecules derived from B cell lymphoma cells  
 XX  
 PS Example 2; Page 108-109; 177pp; English.  
 XX  
 CC This sequence comprises hypoxanthine phosphoribosyltransferase  
 CC (HPRT) from mouse. The HPRT gene (see AAT97166) was utilised in  
 CC the construction of selection vector pMSD5-HPRT, which contains  
 CC full-length HPRT DNA under transcriptional control of the Moloney  
 CC LTR (see also AAT97160). The invention provides vectors and improved  
 CC methods for the expression and co-amplification of genes encoding  
 CC recombinant proteins in cultured cells. The methods permit the  
 CC isolation of cell lines which have co-amplified input recombinant  
 CC sequences which encode an amplifiable marker, one or more  
 CC expression vectors encoding a protein of interest and optionally a  
 CC selectable marker. The amplified cells provide large quantities of  
 CC recombinant proteins suitable for immunotherapy for treatment of  
 CC lymphomas and leukaemias. The methods permit the production of  
 CC custom vaccines, including multivalent vaccines, that reflect the  
 CC degree of somatic variation found in a patient's tumour.

XX Sequence 218 AA;  
 Query Match 69.2%; Score 772; DB 18; Length 218;  
 Best Local Similarity 67.9%; Pred. No. 3.1e-77;  
 Matches 144; Conservative 32; Mismatches 36; Indels 0; Gaps 0;

QY 1 MATRSPGVIMDDPGYDLNFTYPQHYGGDLEVLPHGIIIVDRIERIAKDIMKDIGS 60  
 DB 1 MPTRSPGVISDDPGYDLNFTYPQHYGGDLEVLPHGIIIVDRIERIAKDIMKDIGS 60  
 QY 61 DIMVLVLKGGYKFCADLVEHLKNI SRNSDRFVSMKVD FIRLKS YRNDQSGMGEMQIIIGG 120  
 DB 61 HIVALCVLKGGYKFCADLVEHLKNI SRNSDRFVSMKVD FIRLKS YRNDQSGMGEMQIIIGG 120  
 QY 121 DLSTLAGKNFLIVDVGTGRMTKALLNIEKYKPNMIVKASLLVKRTSRSDGFRPDYAG 180  
 DB 121 DLSTLTGKNVLIVEDIIDTGMTQTLTSLVQYSPKMKVVASLLVKRTSRSGYRDFVG 180  
 QY 181 FEIPLFVVGVALDYNEFRDLNHCIVNEHG 212  
 DB 181 FEIPDKFVVGVALDYNEFRDLNHCIVNEHG 212

RESULT 6  
 AAB85165  
 ID AAB85165 standard; Protein; 231 AA.  
 XX AAB85165;  
 AC AAB85165;  
 DT 07-SEP-2001 (first entry)  
 XX P. falciparum HGPRT enzyme.  
 DE  
 KW Hypoxanthine-guanine phosphoribosyl transferase; HGPRT; enzyme; malaria;  
 KW plasmodium.  
 XX Plasmodium falciparum.  
 OS  
 XX USG248577-B1.  
 EN  
 PD 19-JUN-2001.  
 XX  
 PF 16-JUL-1990; 90US-0552744.  
 XX  
 PR 16-JUL-1990; 90US-0552744.  
 XX  
 PA (SOUR ) SOUTHERN RES INST.  
 XX  
 PI Vasanthakumar G, Montgomery JA;  
 XX





XX Claim 17; SEQ ID NO: 6465; 246pp + Sequence Listing; English.  
 PS The present invention provides a number of nucleotide and protein  
 XX sequences from the Corynebacterium glutamicum glutamicum. These  
 CC are useful for identifying the mutation point of a gene derived from a  
 CC mutant of corynebacterium, measuring expression amount and  
 CC analysing the expression profile or expression pattern of a gene derived  
 CC from corynebacterium, and identifying a homologue of a gene derived  
 CC from corynebacterium. Corynebacterium bacteria are useful for producing  
 CC amino acids, nucleic acids, vitamins, saccharides and organic acids,  
 CC particularly L-lysine. The present sequence is a protein described  
 CC in the exemplification of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from the  
 CC European Patent Office.  
 XX  
 XX Sequence 194 AA;  
 SQ  
 Query Match 22.5%; Score 251.5; DB 22; Length 194;  
 Best Local Similarity 34.3%; Pred. No. 1.6e-19;  
 Matches 69; Conservative 41; Mismatches 68; Indels 23; Gaps 9;  
 QY 18 DLNLFYQHYXG-DLEYVLIPIHGIIVDRIERLAKDIMKDI--GYSDIMVLVKGXKFP 74  
 Db 6 DLNV---PANPYGTIESVLISEELKQRIAEAKVSEFEKDAEDLLIVCVLKGAFIP 62  
 QY 75 CADLVEHLKNIERNDRFVSMKVDIFRLKSYRND-QSMGEMQIIGGDLSTLAGKNFLIV 133  
 Db 63 LAD-----FSRMLD--IPTQSEFMAVSSYGNSTSSGVRILKDL-KEIEGRDVLIV 112  
 QY 134 EDVVTGRTMKALLSNIKYPKMKIKVASLLYK---RTSRSDGFRPDYAGFIPHLFVVG 190  
 Db 113 EDIISGLTSLWMLNKNRNKSNVITLLRKPERLATNIDMFD---IGFDIPNEFVVG 169  
 QY 191 VALDNEYFRDLNHCIVINEH 211  
 Db 170 YGLDFAERYRDLPYVGTLEPH 190  
 RESULT 11  
 ID AAB80144 standard; Protein; 200 AA.  
 AC AAB80144;  
 XX  
 DT 30-APR-2001 (first entry)  
 XX  
 DE Corynebacterium glutamicum MP protein sequence SEQ ID NO:1022.  
 XX  
 KW Corynebacterium glutamicum; metabolic pathway protein; MP protein;  
 KW fine chemical production; microorganism; organic acid; nucleoside;  
 KW nonproteinogenic amino acid; purine base; pyrimidine base; nucleotide;  
 KW lipid; saturated fatty acid; unsaturated fatty acid; diol; vitamin;  
 KW carbohydrate; aromatic compound; cofactor; polyketide; enzyme.  
 XX  
 OS Corynebacterium glutamicum.  
 XX  
 PN WO2000100843-A2.  
 XX  
 PD 04-JAN-2001.  
 XX  
 PF 23-JUN-2000; 2000WO-IB00923.  
 XX  
 PR 25-JUN-1999; 99US-0141031.  
 PR 01-JUL-1999; 99DE-1030476.  
 PR 02-JUL-1999; 99US-0142101.  
 PR 08-JUL-1999; 99DE-1031415.  
 PR 08-JUL-1999; 99DE-1031418.  
 PR 08-JUL-1999; 99DE-1031419.  
 PR 08-JUL-1999; 99DE-1031420.  
 PR 08-JUL-1999; 99DE-1031424.  
 PR 08-JUL-1999; 99DE-1031428.

PR 08-JUL-1999; 99DE-1031434.  
 PR 08-JUL-1999; 99DE-1031435.  
 PR 08-JUL-1999; 99DE-1031443.  
 PR 08-JUL-1999; 99DE-1031453.  
 PR 08-JUL-1999; 99DE-1031457.  
 PR 08-JUL-1999; 99DE-1031465.  
 PR 08-JUL-1999; 99DE-1031478.  
 PR 08-JUL-1999; 99DE-1031510.  
 PR 08-JUL-1999; 99DE-1031541.  
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 PR 08-JUL-1999; 99DE-1031592.  
 PR 08-JUL-1999; 99DE-1031632.  
 PR 08-JUL-1999; 99DE-1031634.  
 PR 08-JUL-1999; 99DE-1031636.  
 PR 09-JUL-1999; 99DE-1032125.  
 PR 09-JUL-1999; 99DE-1032126.  
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 PR 09-JUL-1999; 99DE-1032206.  
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 PR 14-JUL-1999; 99DE-1033005.  
 PR 14-JUL-1999; 99DE-1033006.  
 PR 12-AUG-1999; 99US-0148613.  
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 PR 31-AUG-1999; 99DE-1041380.  
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 PR 31-AUG-1999; 99DE-1041396.  
 PR 03-SEP-1999; 99DE-1042076.  
 PR 03-SEP-1999; 99DE-1042077.  
 PR 03-SEP-1999; 99DE-1042079.  
 PR 03-SEP-1999; 99DE-1042086.  
 PR 03-SEP-1999; 99DE-1042087.  
 PR 03-SEP-1999; 99DE-1042088.  
 PR 03-SEP-1999; 99DE-1042095.  
 PR 03-SEP-1999; 99DE-1042124.  
 PR 03-SEP-1999; 99DE-1042129.  
 PR 09-MAR-2000; 2000US-0187970.  
 XX  
 (BADI ) BASF AG.  
 PA  
 Pompejus M, Kroeger B, Schroeder H, Zelder O, Haberhauer G;  
 PI  
 WPI; 2001-137957/14.  
 DR N-PSDB; AAF72263.  
 XX  
 Nucleic acids from Corynebacterium glutamicum encoding metabolic  
 PT pathway proteins, useful for producing fine chemicals in  
 PT microorganisms, including organic acids, nonproteinogenic amino acids,  
 PT and purine and pyrimidine bases -  
 XX  
 Claim 20; Page 1561-1562; 1737pp; English.  
 PS  
 XX AAF71753 to AAF72330 encode the Corynebacterium glutamicum metabolic  
 CC pathway (MP) proteins given in AAB79634 to AAB80211. The C. glutamicum  
 CC MP nucleic acids are useful for the production of fine chemicals  
 CC in microorganisms, including organic acids, nonproteinogenic amino  
 CC acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids,  
 CC saturated and unsaturated fatty acids, diols, carbohydrates, aromatic  
 CC compounds, vitamins, cofactors, polyketides and enzymes.  
 XX  
 SQ Sequence 200 AA;

```

Query Match      22.5%; Score 251.5; DB 22; Length 200;
Best Local Similarity 34.3%; Pred. No. 1.7e-19;
Matches 69; Conservative 41; Mismatches 68; Indels 23; Gaps 9;

QY 18 DLNLFYPOHYG-DLEVVLPHGIIVDRIERLAKIMKDI--GYSDIMVLCVLKGYKF 74
D 12 DLNV-----PANPYTDIESVLISEKUKQRIAEWAKRVSEEFDAEDLILVLCVLKGAIFY 69
QY 75 CADLVEHLKNISNRDRFVSMKVDIFRLKSYRND-QSMGEMQIIGGGDLSTLAGKNFLIV 133
D 69 LAD-----FSRMLD--IPTQSEFWAVSSYGNTSSGGVRLKDL-DKEIGRDVLIV 118
QY 134 EDVVGTRMTKALLSNIEKYKPNMKVASLLVK---RTSRSDGFRPDYAGFEIPHFLFVVG 190
D 119 EDIIDSGLTSLWMLRNLKRNPKSLNVITLLRKPRLTINIDMFD---IGFDIPNEFVVG 175
QY 191 YALDYNEYFRDLNHNICVINEH 211
D 176 YGLDFAERYRDLFVYGTLEPH 196

RESULT 12
ABB47663
ID ABB47663 standard; Protein; 648 AA.
XX
AC ABB47663;
XX
DT 05-FEB-2002 (first entry)
XX
DE Listeria monocytogenes protein #367.
XX
KW Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
KW vitamin B12; bacterial infection; disease.
XX
OS Listeria monocytogenes.
XX
PN WO200177335-A2.
XX
PD 18-OCT-2001.
XX
PF 11-APR-2001; 2001WO-FR01118.
XX
PR 11-APR-2000; 2000FR-0004629.
XX
PA (INSP ) INST PASTEUR.
XX
PI Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P;
PI Dussurget O, Chetoui F, Nedjari H, Glaser P, Kunst F, Cossart P;
PI Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA;
PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;
PI Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L;
PI Perez-Biaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
PI Maduenio E, De Pablo B, Wehland J, Kaerst U, Entian K, Hauf J;
PI Rose M, Voss H;
XX
WPI; 2002-010914/01.
XX
Genomic sequence for Listeria monocytogenes, useful e.g. for treatment
and prevention of Listeria and related bacterial infections, and
related polypeptides -
XX
Claim 6; SEQ ID No 368; 192pp; French.
XX
The present invention relates to the genome sequence of Listeria
monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of
it are useful for selecting probes and primers for detecting genes in L.
monocytogenes and related organisms, and for studying genetic
polymorphisms and related organisms. The present sequence is a protein
encoded by the genome sequence of the present invention. Proteins
expressed from the genome sequence are useful for raising specific
antibodies, identification of L. monocytogenes and related organisms, and
for biosynthesis and biodegradation, especially biosynthesis of Vitamin
CC
```

```

CC B12. The genome sequence and proteins encoded by it are also useful for
CC selecting compounds that regulate gene expression and cell replication
CC and modulate L. monocytogenes-related diseases. In addition, the genome
CC sequence and proteins encoded by it are useful in pharmaceutical and
CC vaccines compositions for the treatment or prevention of infections by L.
CC monocytogenes and related organisms.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 648 AA;

Query Match      22.4%; Score 250.5; DB 23; Length 648;
Best Local Similarity 33.0%; Pred. No. 1.1e-18;
Matches 60; Conservative 46; Mismatches 63; Indels 13; Gaps 5;

QY 29 YGDLEVLVPHGIIVDRIERLAKIMKDIKIDGYSIDIMVLCVLKGYKFCADLVEHLKNISRN 88
D 471 HNDIQVLISEDELOEKIRELGRELTEYEGRNPLVGVLGKATPFMTDLKRV----- 524
QY 89 SDRFVSMKVDIFRLKSYRNDQ-SMGEMQIIGGGDL-STLAGKNFLIVEDVVGTRMTKAL 146
D 525 -DTYLEM--DFMDVSSYGNGTVSSGEVKII--KDLNASVEGRDVLVIEDIIDSRTLSTYL 579
QY 147 LSNIEKYKPNMKVASLLVKTSSDGRPDYAGFEIPHFLFVVGALDYNEYFRDLNHNIC 206
D 580 VDLIKYRKAKSVKLVTLDDPKAGRNVIEADYVGVFVVPNEFVVGVDYAEYRNLPYIG 639
QY 207 VI 208
D 640 IL 641

RESULT 13
AAW80653
ID AAW80653 standard; Protein; 180 AA.
XX
AC AAW80653;
XX
DT 24-DEC-1998 (first entry)
XX
DE S. pneumoniae putative ATPase involved in membrane functions.
XX
KW Streptococcus pneumoniae protein; recombinant; gene expression; DNA chip;
KW virulence; antibody; infection; detection; treatment; hypothetical;
KW cell wall biosynthetic, external target; minimal gene set protein.
XX
OS Streptococcus pneumoniae.
XX
PN WO9826072-A1.
XX
PD 18-JUN-1998.
XX
PF 09-DEC-1997; 97WO-US22578.
XX
PR 13-DEC-1996; 96US-0036281.
XX
PA (ELIL ) LILLY & CO ELI.
XX
PI Baltz RH, Burgett SG, Dehoff BS, Hoskins JA, Jaskunas SR;
PI Mills BJ, Norris FH, Peery RB, Rockey PK, Rostock PR;
PI Skatrud PL, Smith MC, Solenberg PJ, Treadway PJ;
XX
WPI; 1998-348529/30.
DR N-PSDB; AAV65227.
XX
Streptococcus pneumoniae nucleic acid sequences - used in DNA chips
for evaluating gene expression, and identification of virulence
PT genes
XX
PS Claim 3; Pages 239-240; 333pp; English.
XX
```







GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 13, 2003, 15:04:11 ; Search time 21 Seconds  
(without alignments)  
427.138 Million cell updates/sec

Title: US-09-902-705-2

Perfect score: 1116

Sequence: 1 MATRSPGVIMDDWPGVDLN.....LDYNEPRDLNHCIVINEHG 212

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pap:\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pap:\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pap:\*  
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5: /cgn2\_6/ptodata/1/iaa/PTCUS\_COMB.pap:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1069	95.8	225	4	US-09-786-240-4
2	772	69.2	218	1	US-08-644-664B-14
3	772	69.2	218	2	US-08-761-277A-14
4	263.5	23.6	200	4	US-09-107-532A-4646
5	238.5	21.4	181	4	US-09-134-001C-3318
6	190	17.0	178	4	US-09-328-352-4965
7	157	14.1	214	4	US-09-252-991A-30612
8	119	10.7	179	4	US-09-107-532A-5030
9	96	8.6	182	4	US-08-920-803A-2
10	96	8.6	182	4	US-08-920-803A-4
11	89	8.0	187	4	US-09-134-001C-4780
12	88.5	7.9	1028	4	US-09-328-352-5749
13	87	7.8	494	3	US-08-993-250-3
14	87	7.8	892	1	US-07-977-434-12
15	87	7.8	892	1	US-08-458-819-12
16	87	7.8	892	5	PCT-US91-07035-12
17	84.5	7.6	207	4	US-09-252-991A-17055
18	84.5	7.6	272	4	US-09-107-532A-5898
19	82	7.3	834	4	US-09-252-991A-31321
20	78.5	7.0	403	4	US-09-134-001C-4797
21	78.5	7.0	419	4	US-09-134-001C-5077
22	78.5	7.0	419	4	US-09-328-352-6451
23	78	7.0	1038	3	US-09-541-782-4
24	78	7.0	1038	4	US-09-723-820-4
25	77	6.9	503	4	US-08-252-991A-32777
26	77	6.9	1169	1	US-08-315-468-4
27	75.5	6.8	1218	4	US-09-589-567-2

28	75	6.7	641	4	US-09-724-623-76	Sequence 76, Appl
29	74.5	6.7	285	3	US-09-327-681-6	Sequence 6, Appl
30	74.5	6.7	1454	4	US-09-328-352-5793	Sequence 5793, Ap
31	74	6.6	420	4	US-09-107-532A-4045	Sequence 4045, Ap
32	73.5	6.6	287	4	US-09-107-532A-4530	Sequence 4530, Ap
33	73.5	6.6	313	4	US-09-134-001C-5621	Sequence 5621, Ap
34	73	6.5	329	4	US-09-107-532A-4092	Sequence 4092, Ap
35	72.5	6.5	375	4	US-09-107-532A-5089	Sequence 5089, Ap
36	72.5	6.5	943	1	US-08-455-970A-10	Sequence 10, Appl
37	72	6.5	396	3	US-09-273-686-2	Sequence 2, Appl
38	71.5	6.4	362	4	US-09-252-991A-31766	Sequence 31766, A
39	71.5	6.4	480	4	US-09-252-991A-28668	Sequence 28668, A
40	71.5	6.4	566	2	US-08-920-095-3	Sequence 3, Appl
41	71.5	6.4	566	5	PCT-US96-05800-3	Sequence 3, Appl
42	71.5	6.4	569	2	US-08-467-822-26	Sequence 26, Appl
43	71.5	6.4	569	3	US-08-432-697-26	Sequence 26, Appl
44	71.5	6.4	569	3	US-08-466-248-26	Sequence 26, Appl
45	71.5	6.4	777	1	US-08-526-964-3	Sequence 3, Appl

## ALIGNMENTS

### RESULT 1

US-09-786-240-4  
; Sequence 4, Application US/09786240  
; Patent No. 6558935  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE PHARMACEUTICALS, INC.  
; APPLICANT: TANG, Y. Tom  
; APPLICANT: CORLEY, Neil C.  
; APPLICANT: GUEGLER, Karl J.  
; APPLICANT: BAUGHN, Mariah R.  
; APPLICANT: LAL, Preeti  
; APPLICANT: YUE, Henry  
; APPLICANT: HILLMAN, Jennifer L.  
; APPLICANT: AZIMZAI, Valda  
; TITLE OF INVENTION: HUMAN TRANSFERASE PROTEINS  
; FILE REFERENCE: PF-0592 PCT  
; CURRENT APPLICATION NUMBER: US/09/786,240  
; CURRENT FILING DATE: 2002-03-12  
; PRIOR APPLICATION NUMBER: 09/150,657; unassigned; 09/186,779; unassigned; 60/133,642  
; PRIOR FILING DATE: 1998-09-10; 1998-09-10; 1998-11-04; 1998-11-04; 1999-05-11  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PERL Program  
; SEQ ID NO 4  
; LENGTH: 225  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc.feature  
; OTHER INFORMATION: Incyte ID No. 6558935 1404963CD1  
US-09-786-240-4

Query Match 95.8%; Score 1069; DB 4; Length 225;  
Best Local Similarity 98.5%; Pred. No. 1.8e-119;  
Matches 203; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy	7	GVWIMDWP	GVYDLNLF	TPYQHYG	DLEVLPH	GIIVDR	IERLAKD	IMKDIG	SDIMVLC	66
Db	14	GVWIMDWP	GVYDLNLF	TPYQHYG	DLEVLPH	GIIVDR	IERLAKD	IMKDIG	SDIMVLC	73
Qy	67	VLKGGYK	FACDLV	EHKLN	ISNSDR	FVSMK	VDFIRL	KSYRND	QSMGENQ	126
Db	74	VLKGGYK	FACDLV	EHKLN	ISNSDR	FVSMK	VDFIRL	KSYRND	QSMGENQ	133
Qy	127	GKNFLI	VEDVVG	TGRTMK	ALLSNIE	KYKPN	MKVAS	LLVKTS	SDGFRPPY	186
Db	134	GKNFLI	VEDVVG	TGRTMK	ALLSNIE	KYKPN	MKVAS	LLVKTS	SDGFRPPY	193
Qy	187	FVVG	YALD	YNEFR	DLNHC	IVINE	HEHG	212		
Db	194	FVVG	YALD	YNEFR	DLNHC	IVINE	HEHG	219		

```

RESULT 2
US-08-644-664B-14
; Sequence 14, Application US/08644664B
; Patent No. 5776746
; GENERAL INFORMATION:
; APPLICANT: Denney Jr., Dan W.
; TITLE OF INVENTION: Gene Amplification Methods
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States Of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/644,664B
; FILING DATE: 01-MAY-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ingolia, Diane B.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: GENITOPE-00912
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-644-664B-14

Query Match 69.2%; Score 772; DB 1; Length 218;
Best Local Similarity 67.9%; Pred. No. 5.3e-84;
Matches 144; Conservative 32; Mismatches 36; Indels 0; Gaps 0;

QY 1 MATRSPGVIMDDPQYDNLNFTYPOHYGDLVLIPIHGIIVDRIERLAKDIMKDIGYS 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 MPTRSPSVVISDDEPGYDLDFCIPNHYAEDLEKVFIPHGLIMDRTERLARDVMEKMGH 60

QY 61 DIMVLCVLKGGYKFCADLVEHLKNI SRNSDRFVSMKVDFIRLKS YRNDOSMGEMQIIGG 120
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
61 HIVALCVLKGKGFADLDYIKALNRNSDRSIPMTVDFIRLKS YCNDOSTGDIKVIGD 120

QY 121 DLSTLAGKNFLIVEDVVGTRTKALLSNI EKYPKNMKIVASLLVKRTSRSDGFRPDYAG 180
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
121 DLSTLTGKNVLIVEDIIDTGKTMQTL LSLVKQYSPKQWKVASLLVKRTSRSGYRPFV 180

QY 181 FEIPLFVVGVALDYNEFRDLNHCIVNEHG 212
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
181 FEIPDKFVVGVALDYNEFRNLNHCIVSETG 212

RESULT 3
US-08-761-277A-14
; Sequence 14, Application US/08761277A
; Patent No. 5972334
; GENERAL INFORMATION:
; APPLICANT: Denney Jr., Dan W.
; TITLE OF INVENTION: Vaccines For Treatment Of Lymphoma And
; TITLE OF INVENTION: Leukemia
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP

```

```

; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States Of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/761,277A
; FILING DATE: 06-DEC-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/644,664
; FILING DATE: 01-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: GENITOPE-02406
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-761-277A-14

Query Match 69.2%; Score 772; DB 2; Length 218;
Best Local Similarity 67.9%; Pred. No. 5.3e-84;
Matches 144; Conservative 32; Mismatches 36; Indels 0; Gaps 0;

QY 1 MATRSPGVIMDDPQYDNLNFTYPOHYGDLVLIPIHGIIVDRIERLAKDIMKDIGYS 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 MPTRSPSVVISDDEPGYDLDFCIPNHYAEDLEKVFIPHGLIMDRTERLARDVMEKMGH 60

QY 61 DIMVLCVLKGGYKFCADLVEHLKNI SRNSDRFVSMKVDFIRLKS YRNDOSMGEMQIIGG 120
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
61 HIVALCVLKGKGFADLDYIKALNRNSDRSIPMTVDFIRLKS YCNDOSTGDIKVIGD 120

QY 121 DLSTLAGKNFLIVEDVVGTRTKALLSNI EKYPKNMKIVASLLVKRTSRSDGFRPDYAG 180
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
121 DLSTLTGKNVLIVEDIIDTGKTMQTL LSLVKQYSPKQWKVASLLVKRTSRSGYRPFV 180

QY 181 FEIPLFVVGVALDYNEFRDLNHCIVNEHG 212
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
181 FEIPDKFVVGVALDYNEFRNLNHCIVSETG 212

RESULT 4
US-09-107-532A-4646
; Sequence 4646, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>

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;
; SOFTWARE: ASCII
;
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/107,532A
;   FILING DATE: 30-Jun-1998
;
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 60/085,598
;   FILING DATE: 14 May 1998
;   APPLICATION NUMBER: 60/051571
;   FILING DATE: July 2, 1997
;
; ATTORNEY/AGENT INFORMATION:
;   NAME: Ariniello, Pamela Deneka
;   REGISTRATION NUMBER: 40,489
;   REFERENCE/DOCKET NUMBER: GTC-012
;
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (781)893-5007
;   TELEFAX: (781)893-8277
;
; INFORMATION FOR SEQ ID NO: 4646:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 200 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   HYPOTHETICAL: YES
;   ORIGINAL SOURCE:
;     ORGANISM: Enterococcus faecium
;
; FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (B) LOCATION 1...200
;   SEQUENCE DESCRIPTION: SEQ ID NO: 4646:
US-09-107-532A-4646

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Query Match      23.6%; Score 263.5; DB 4; Length 200;
Best Local Similarity 38.1%; Pred. No. 2.6e-23;
Matches 69; Conservative 39; Mismatches 58; Indels 15; Gaps 7;

QY 31 DLEYVLIPIHGIIVDRIERIAKDIMKDIGYSDIMVLCVKGKFCADLVEHLKNISRNSD 90
Db 24 DIERILISQEEIQVACKELGKELTEIYQNTNPLVGVLLKGAVPFVADIV-----RSID 76

QY 91 RFVSKMVDPIRLKSYRN-DQSGEMQIIGGGDLST-LAGKNFLIVEDVVGTRTKALLS 148
Db 77 TY--LELDFMDVSSYGATVSSGEVKIV--KDLDTNVEGRDLLIVEDIIDSGRT-RAYIV 131

QY 149 NIEKY-KENMLKVASLLVKRTSRSDGFRPDYAGFEIPLHFLVVGVALDYNVFRDLNHICV 207
Db 132 DLFKTRAKSVKIVTLDDKREGVVNIEADYVGFNVPNEFVVGGLDYAEAYRNLPYIGV 191

QY 208 I 208
Db 192 L 192

```

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RESULT 5
US-09-134-001C-3318
; Sequence 3318, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3318
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3318

```

```

Query Match      21.4%; Score 238.5; DB 4; Length 181;
Best Local Similarity 33.5%; Pred. No. 2.2e-20;
Matches 62; Conservative 38; Mismatches 56; Indels 29; Gaps 7;

QY 31 DLEYVLIPIHGIIVDRIERIAKDIMKDIG-----YSDIMVLCV--LKGKFKFCADLVEHL 82
Db 6 DLKNVLLS-----EEDIQNICEMGAIITEDYKDRPLVCVGLKGSVMFMADLIKRI 57

QY 83 KNISNRSDRFVSMKVDPIRLKSYR-NDQSGEMQIIGGGDL-STLAGKNFLIVEDVVGTVG 140
Db 58 D-----THLSIDFMDVSSYHGTESTGEVQIL--KDLGASIKNKVLIIEDILETG 106

QY 141 RTMKALLSNIIEKYKPNMKIVASLLVKRTSRSDGFRPDYAGFEIPLHFLVVGVALDYNVEYR 200
Db 107 TTLKSIITELQSRKYNLSLEIATLLDKPNRRKADIEAKYVVGKKIPDEFVVGGLDYRELYR 166

QY 201 DLNHI 205
Db 167 NLPYI 171

RESULT 6
US-09-328-352-4965
; Sequence 4965, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4965
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4965

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```

Query Match      17.0%; Score 190; DB 4; Length 178;
Best Local Similarity 26.0%; Pred. No. 1.3e-14;
Matches 50; Conservative 44; Mismatches 60; Indels 38; Gaps 6;

QY 35 VLIPIHGIIVDRIERIAKDIMKDIGYSD--IMVLCVLLKGGYKFCADLVEHLKNISNRDRF 92
Db 10 IMISTEEIQAKVKELGEGQINSHYANSDELVLIGLLRGSVIFMADL---CRITIKPHE-- 64

QY 93 VSMKVDPIRLKSYRNDQSGEMQIIGGGDLST-----LAGKNFLIVEDVVGTVG 140
Db 65 ---LDFMTVSSY-----GGTTSRDVKILKLDLGEIRGKDVLVVEDIIDSG 108

QY 141 RTMKALLSNIIEKYKPNMKIVASLLVKRTSRSDGFRPDYAGFEIPLHFLVVGVALDYNVEYR 200
Db 109 NTLKSVEMLOTREPNSIQCLTLVSKPSRRREIDLEVFLGFEVEDKFIYVGLDYDQKYR 168

QY 201 DLNHICVINEHG 212
Db 169 ---HLPFIGEIG 177

```

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RESULT 7
US-09-252-991A-30612
; Sequence 30612, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788

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```

; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...179
; SEQUENCE DESCRIPTION: SEQ ID NO: 5030
US-09-107-532A-5030

Query Match 10.7%; Score 119; DB 4; Length 179;
Best Local Similarity 25.5%; Pred. No. 4.1e-06;
Matches 39; Conservative 37; Mismatches 61; Indels 16; Gaps

QY 42 IVPRI-----ERLAKDIM-KDIGYSDIMVLVLKGGYKFCADLVHLKKNISRNSDRFVS 94
Db 6 VVDQVTKRALTRITYEIIERNHSIQIDVLVGKTRGIYIASRIAERLKLQLED-----ID 60
QY 95 MKYDFILKSYRNDQSMG-ENQIIGGGDLS-TLAKKNFLIVEDVYGTGTMKALLSNIEK 152
Db 61 IPVGELDITLYRDDKKNPEPEPELHSSDIPVSLGKKEVILIDDDVLYTGRTIRAAAMDAMD 120
QY 153 Y-KPNMIKVASLLVKTRSRSDGFRPDYAGFEIP 184
Db 121 FGRPRKISLA-VLVDRGHRELPIRADYVGKNIP 152

RESULT 9
US-08-920-803A-2
; Sequence 2, Application US/08920803A
; Patent No. 6331410
; GENERAL INFORMATION:
; APPLICANT: Burnham, Martin T.
; APPLICANT: Lonetto, Michael A.
; APPLICANT: Warren, Patrick V.
; TITLE OF INVENTION: NO. 6331410e1 pyR Homolog
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert, Price & Rhoads
; STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2793
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/920,803A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dickinson, Q. Todd
; REGISTRATION NUMBER: 28,354
; REFERENCE/DOCKET NUMBER: GM10086
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215/994-2252
; TELEFAX: 215/994-2222
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 182 amino acids
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-920-803A-2

Query Match 8.6%; Score 96; DB 4; Length 182;
Best Local Similarity 25.8%; Pred. No. 0.0024;
Matches 40; Conservative 36; Mismatches 71; Indels 8; Gaps 6
QY 33 EYVLPHGIIVDRIERLAKDIMKDIGYSDITMVLVLKGGYKFCADLVHLKKNISRNSDRF 92

```

```
Db 3 ERIIMDDAAIORTVTRIAHEILEYKNGTDNLLILGIKTRGEYLANIOTD-KIHQIEQORI 61
Qy 93 VSMKVDIFRLKSYND-QSMGEMQIIGGGDLST-LAGKNFLIVEDVVGRTMTKALLSNI 150
Db 62 PTGTID---ITYFRDDIEHMSLTTKDAIDIDTIDTKWIIIDDVLYTGRTVRASLDAI 118
Qy 151 -EKYKPNMKIVASLLVKRTSRSDGFRPDYAGFEIP 184
Db 119 LLNARPIKIGLAA-LVDRGHRLEPIRADFVGKNIP 152

RESULT 10
US-08-920-803A-4
; Sequence 4, Application US/08920803A
; Patent No. 6331410
; GENERAL INFORMATION:
; APPLICANT: Burnham, Martin T.
; APPLICANT: Lonetto, Michael A.
; APPLICANT: Warren, Patrick V.
; TITLE OF INVENTION: No. 6331410el pyrR Homolog
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert, Price & Rhoads
; STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2793
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/08/920.803A
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dickinson, Q. Todd
; REGISTRATION NUMBER: 28,354
; REFERENCE/DOCKET NUMBER: GM10086
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215/994-2252
; TELEFAX: 215/994-2222
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 182 amino acids
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-920-803A-4

Query Match
Best Local Similarity 8.6%; Score 96; DB 4; Length 182;
Matches 40; Conservative 36; Mismatches 71; Indels 8; Gaps 6;

Qy 33 EYVLPHGIIVDRIERLAKDIMKDIGYSDIMVLCVLKGGYKFCADLVEHLKNI SRNSDRF 92
Db 3 ERIIMDDAAIORTVTRIAHEILEYKNGTDNLLILGIKTRGEYLANIOTD-KIHQIEQORI 61
Qy 93 VSMKVDIFRLKSYND-QSMGEMQIIGGGDLST-LAGKNFLIVEDVVGRTMTKALLSNI 150
Db 62 PTGTID---ITYFRDDIEHMSLTTKDAIDIDTIDTKWIIIDDVLYTGRTVRASLDAI 118
Qy 151 -EKYKPNMKIVASLLVKRTSRSDGFRPDYAGFEIP 184
Db 119 LLNARPIKIGLAA-LVDRGHRLEPIRADFVGKNIP 152
```

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RESULT 11
US-09-134-001C-4780
; Sequence 4780, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: GTC-007
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4780
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4780

Query Match
Best Local Similarity 8.0%; Score 89; DB 4; Length 187;
Matches 41; Conservative 31; Mismatches 31; Indels 18; Gaps 6;

Qy 33 EYVLPHGIIVDRIERLAKDIMK-DIGYSDIMVLCVLKGGYKFCADLVEHLKNI SRNSDR 91
Db 15 ERIILDEAAIORTTITRIAEILEYKNGTKDLVLL-----GIKTRGAFLAHRTQDKINSIE 69
Qy 92 FVSMKVDIFRLKSYNDQSMGEMQIIGGGDLST-----LAGKNFLIVEDVVGRTMTKA 145
Db 70 QQLVPTGTIDITHFRDDVD---KVVQADQYAFEDINNNKVVIIIDDLVLTGRTVRA 125
Qy 146 LLSNIEKY-KPNMIKVASLLVKRTSRSDGFRPDYAGFEIP 184
Db 126 SLDAILLHTRPIKIGLAA-LVDRGHRLEPIRADFVGKNIP 164

RESULT 12
US-09-328-352-5749
; Sequence 5749, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5749
; LENGTH: 1028
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5749

Query Match
Best Local Similarity 7.9%; Score 88.5; DB 4; Length 1028;
Matches 34; Conservative 42; Mismatches 61; Indels 25; Gaps 7;

Qy 33 EYVLPHGIIVDRIERLAKDIMKDIGYSDIMVLCVLKGGYKFCADLVEHLKNI SRNSDRF 92
Db 594 ELDIAP-GVKASKVTNISRLARSMSASVRVVEIPGKPYIGIEV-----PNSARE 644
Qy 93 VSMKVDIFRLKSYNDQSMGEM-----QIIGGGDLSTLAGKNFLIVEDVVGRTM---KA 145
Db 645 MVRLLIELETFAYDPSPALISMANGKDISGNPVLTDLAKAPHMLVAGTTGSGKSVAVNSM 704
Qy 146 LLSNIEKYKPNMIKVASLLVKRTSRSDGFRPDYAGF-EIPIHL 186
Db 705 ILSMLLKYTDPQLRL--ILI-----DPKQLELANYNIDPHL 738
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RESULT 13
US-09-902-705-2
; Sequence 3, Application US/08993260
; Patent No. 6031089
; GENERAL INFORMATION:
; APPLICANT: Bienkowski, Michael J.
; TITLE OF INVENTION: No. 6031089el Sequences of p56, a Proteins Which
; TITLE OF INVENTION: Affects K-ATP Channels
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pharmacia and Upjohn, Co., Intel. Prop. Law
; ADDRESS: (1920-32-LAW)
; STREET: 301 Henrietta Street
; CITY: Kalamazoo
; STATE: Michigan
; COUNTRY: U.S.A.
; ZIP: 49001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/993,260
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wootton, Thomas A.
; REGISTRATION NUMBER: 35,004
; REFERENCE/DOCKET NUMBER: 6092
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (616) 833-7914
; TELEFAX: (616) 833-8897
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 494 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; US-09-902-705-2
Query Match 7.8%; Score 87; DB 3; Length 494;
Best Local Similarity 20.4%; Pred. No. 0.13;
Matches 56; Conservative 38; Mismatches 84; Indels 96; Gaps 13;
Qy 13 DWPGYDNLFTYPOHYGDLBYLPHGIIVDRIERIAKDIKIDYSDIMVLCKGGY 72
Db 124 DW--YLLNLFRLMWHY-----GISFLQMMVEEYVNEKF---MEIKYQAHGY 166
Qy 73 KFCADLVHGL-----KNISRNS-----DRFVSMKVDPFIRLKSRYNDQSM- 111
Db 167 AFSG--VEELYSIGESTFVNMTQSHVAESLLQGVGTORFIDDDVVSALVRSYQGSAMP 224
Qy 112 ---GEMQIIGG-GDLSTLAGNFIIVEDV--VGRTRTKALLSNIKYKP----- 155
Db 225 AFAGMSIAGAQGSLWSVEGGNKLKVCGLLTKLVANVIAHTVSTLHSTGKALYQVAY 284
Qy 156 -----NMKVASLIVKTRSRD-----GFRP-----D 177
Db 285 ENEVGNSSDFYDVIIVATPLPLDNLSSNNLTAFGHPFPIDDDVQGSFQPTWSLVHGLNLS 344
Qy 178 YAGFEIPLHFLVGVYAL--DYNEFRDLNHIQVIN 209
Db 345 YFGPPDKPLFPANILITDFPSFCTLDNICPVN 378
RESULT 14
US-07-977-434-12
```

```

; Sequence 12, Application US/07977434
; Patent No. 5466591
; GENERAL INFORMATION:
; APPLICANT: Gelfand, David H.
; APPLICANT: Abramson, Richard D.
; TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
; TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: 7
; SOFTWARE: WordPerfect 2.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/977,434
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 590,490
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 590,466
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 590,213
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 523,394
; FILING DATE: 15-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 143,441
; FILING DATE: 12-JAN-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 063,509
; FILING DATE: 17-JUN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,241
; FILING DATE: 22-AUG-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 746,121
; FILING DATE: 15-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US90/07641
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 585,471
; FILING DATE: 20-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 455,611
; FILING DATE: 22-DEC-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 609,157
; FILING DATE: 02-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 557,517
; FILING DATE: 24-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Luann Cseri
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: Case No. 5466591 8753
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2972
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 892 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
```



```
; MOLECULE TYPE: protein
US-07-977-434-12

Query Match      7.8%; Score 87; DB 1; Length 892;
Best Local Similarity 20.7%; Pred. No. 0.33;
Matches 45; Conservative 41; Mismatches 73; Indels 58; Gaps 10;

QY 29 YGDLEYVLIPIHGIIIVDRIERLAKDIMKDI-----GYSDIM 63
DB 212 YNSLENVLKNNLLTEKLRRLLEDSKDLQKSIELVELIYDVPMDVEKDEIIRGYNPDK 271
QY 64 VLVKLGKGYKFC-----DLVEHLKN---ISRNSDRFVSMKVDFIRLKSYNRNDQSMG--- 112
DB 272 LLKVLK-KYFSSIIKEINLQKLEKEVILVDNEDKLKLAEEIEKYKTFSDTETTSLD 330
QY 113 --EMQIIGGDLSTLAGNFLIVEDVGTGRMTKALLSNIEKYKPNMKVASLLVKRTS- 169
DB 331 PFEAKLV-GISISTMEGRAYIPVSHFGAKNISKSL---IDKFLKQILQEKDYNIWGQNL 386
QY 170 -----RSDGFRPDYAGFEIPEHL--FVVGVALDYNE 197
DB 387 KFDYEIFKSMGFSPN-----VPHFDTMTIAAYLLNPDE 418

Search completed: November 13, 2003, 15:07:26
Job time : 22 secs

; APPLICATION NUMBER: US 746,121
; FILING DATE: 15-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US90/07641
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 585,471
; FILING DATE: 20-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 455,611
; FILING DATE: 22-DEC-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 609,157
; FILING DATE: 02-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 557,517
; FILING DATE: 24-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Luann Cserr
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: Case No. 5795762 8753
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2972
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 892 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-458-819-12

Query Match      7.8%; Score 87; DB 1; Length 892;
Best Local Similarity 20.7%; Pred. No. 0.33;
Matches 45; Conservative 41; Mismatches 73; Indels 58; Gaps 10;

QY 29 YGDLEYVLIPIHGIIIVDRIERLAKDIMKDI-----GYSDIM 63
DB 212 YNSLENVLKNNLLTEKLRRLLEDSKDLQKSIELVELIYDVPMDVEKDEIIRGYNPDK 271
QY 64 VLVKLGKGYKFC-----DLVEHLKN---ISRNSDRFVSMKVDFIRLKSYNRNDQSMG--- 112
DB 272 LLKVLK-KYFSSIIKEINLQKLEKEVILVDNEDKLKLAEEIEKYKTFSDTETTSLD 330
QY 113 --EMQIIGGDLSTLAGNFLIVEDVGTGRMTKALLSNIEKYKPNMKVASLLVKRTS- 169
DB 331 PFEAKLV-GISISTMEGRAYIPVSHFGAKNISKSL---IDKFLKQILQEKDYNIWGQNL 386
QY 170 -----RSDGFRPDYAGFEIPEHL--FVVGVALDYNE 197
DB 387 KFDYEIFKSMGFSPN-----VPHFDTMTIAAYLLNPDE 418

RESULT 15
US-08-458-819-12
; Sequence 12, Application US/08458819
; Patent No. 5795762
; GENERAL INFORMATION:
; APPLICANT: Gelfand, David H.
; APPLICANT: Abramson, Richard D.
; TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
; TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: 7
; SOFTWARE: Wordperfect 2.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,819
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/977,434
; FILING DATE: 23-FEB-1993
; APPLICATION NUMBER: US 590,490
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 590,466
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 590,213
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 523,394
; FILING DATE: 15-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 143,441
; FILING DATE: 12-JAN-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 063,509
; FILING DATE: 17-JUN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,241
; FILING DATE: 22-AUG-1986
; PRIOR APPLICATION DATA:
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```

; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-925-664-14

Query Match      69.2%; Score 772; DB 10; Length 218;
Best Local Similarity 67.9%; Pred. No. 2.1e-77;
Matches 144; Conservative 32; Mismatches 36; Indels 0; Gaps 0;

QY 1 MATRSPGVIMDDWPGYDLNLFYTPQHYGGDLEYVLPHGIIVDRIERLAKDIMKDIGYS 60
DB 1 MPTRSPSVISDEPGYDLNLFYTPQHYGGDLEYVLPHGIIVDRIERLAKDIMKDIGYS 60
QY 61 DIMVLVLKGGYKFCADLVEHLKNI SRNSDRFVSMKVD FIRLSYRNDQSMGEMOIIIGGG 120
DB 61 HIVALCVLKGKGFADLLDYIKALNRNSDRSIPMTVDFIRLSYRNDQSGTGDIKVIIGD 120
QY 121 DLSTLAGKNFLIVDVGTGRTMKALLSNI EYKPNMIKVASLLVKTSSRSGFPRPDYAG 180
DB 121 DLSTLTGKNVLIVEDIIDTGKTMQTLISLVKQSPRMVKVVASLLVKTSSRSGVPRDFVG 180
QY 181 FEIPLHFLVVGVALDYNEYFRDLNHLHCIVINEHG 212
DB 181 FEIPDKFVVGVALDYNEYFRDLNHLHCIVISGTG 212

RESULT 9
US-09-189-833B-9
; Sequence 9, Application US/09189833B
; Patent No. US20020085393A1
; GENERAL INFORMATION:
; APPLICANT: Bednarik et al.
; TITLE OF INVENTION: Human Hypoxanthine- (Guanine) Phosphoribosyl Transferase-2
; CURRENT APPLICATION NUMBER: US/09/189,833B
; CURRENT FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 08/461,031
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: PCT/US94/11914
; PRIOR FILING DATE: 1994-10-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-09-189-833B-9

Query Match      40.0%; Score 446.5; DB 9; Length 231;
Best Local Similarity 42.7%; Pred. No. 3e-41;
Matches 93; Conservative 41; Mismatches 73; Indels 11; Gaps 3;

QY 5 SPGV-----VIMDDWPGYDLNLFYTPQHYGGDLEYVLPHGIIVDRIERLAKDIMKDI 57
DB 6 NPGAGENAFDPVFVKDDGDDYLDSEFMI PAHYKKYLT KVLVPNGVKNRIEKLAYDIKKVY 65
QY 58 GYSIDIMVLVLKGGYKFCADLVEHLKNI SRNSDRFVSMKV---DFIRLSYRNDQSMGEM 114
DB 66 NNEEFHILCLLKSGRGFTALLKHLSRHNYSAVEMSKPLFGEHYVRVKSVCNDQSTGTL 125
QY 115 QIIGGGDLSTLAGKNFLIVDVGTGRTMKALLSNI EYKPNMIKVASLLVKTSSRSGDF 174
DB 126 EIV-SEDLSCLGKGHVLIVEDIIDTGKTLVKFCEYLKKEIKTVAIACLFIKRTPLWNGF 184
QY 175 RPDYAGFEIPLHFLVVGVALDYNEYFRDLNHLHCIVINEHG 212
DB 185 KADVFVGFIPDFHVVVGYSLDYNEIFRDLHCHCLVNDG 222

RESULT 11
US-10-102-143-13
; Sequence 13, Application US/10102143
; Publication No. US20030185851A1
; GENERAL INFORMATION:
; APPLICANT: Soldati, Dominique
; APPLICANT: Meissner, Markus
; TITLE OF INVENTION: TET transactivator system
; FILE REFERENCE: 04630/016001
; CURRENT APPLICATION NUMBER: US/10/102,143
; CURRENT FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pTetO7Sag1-HXGPRT
US-10-102-143-13

Query Match      30.4%; Score 339; DB 12; Length 230;
Best Local Similarity 34.4%; Pred. No. 2.5e-29;
Matches 67; Conservative 50; Mismatches 76; Indels 2; Gaps 2;

QY 17 YDLNLFYTPQHYGGDLEYVLPHGIIVDRIERLAKDIMKDIIMKDIIMKDIIMKDI 76
DB 28 YNADDPLVPPECKPYIDKILLPGGLVKDRVEKLAYDIHRTYFGBELHICILKSGRGFFN 87
QY 77 DLVEHLKNI SRNSDRFVSMKVD-FIRLSYRNDQSMGEMQIIGGGDLSTLAGKNFLIVED 135

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Db      88 LLIDYLAIONGREGSVPPFFHHYVRLKSYQNDNSTGQUTVL--SDLSIFRDKHVLIVED 146
Qy      136 VVGTRTKALLSNIEKYKPNMKIVASLLVKTSTSDGRPDYAGFEIPLHFLVWGVYALDY 195
Db      147 IVDTGFTLTFEGERLKAQVGPMSRIATLVEKTRDSNSLKGDFVGFSDIEDVWIVGCCYDF 206
Qy      196 NEYFRDLNHNICVINE 210
Db      207 NEMFRDFDHVAVLS 221

RESULT 12
US-09-738-626-6465
; Sequence 6465, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 6465
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6465

Query Match      22.5%; Score 251.5; DB 10; Length 194;
Best Local Similarity 34.3%; Pred. No. 1e-19;
Matches 69; Conservative 41; Mismatches 68; Indels 23; Gaps 9;

Qy      18 DLNFTYPOHYVG-DLEVVLPHGIIVDRIERLAKDIMKDI--GYSDIMVLCVLKGGYKF 74
Db      6 DLNV---PANPYGTDIESVLISEEKLKORIAEMAKRVSEEFKDAEEDLILVCVLKGAFYF 62
Qy      75 CADLVEHLKNTSRSDRFVSMKVPFIRLKSRYND--QSMGEMQIIGGGDLSTLAGKNFLIV 133
Db      63 LAD-----FSRMLD--IPTQSEFMAVSSYGNSTSSGGVRLKLDL-KIEGRDVLIV 112
Qy      134 EDVVGTRTKALLSNIEKYKPNMKIVASLLV---RTSRSDGRPDYAGFEIPLHFLVVG 190
Db      113 EDIISDGLTSLWLNRLKNRPKSLNVITLLRKPERLTNIDMFD---IGFDIPNEFVVG 169
Qy      191 YALDINEYFRDLNHNICVINEH 211
Db      170 YGLDFAERYRDLPVVGTILEPH 190

RESULT 13
US-10-156-761-12199
; Sequence 12199, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO

; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 12199
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-12199

Query Match      20.9%; Score 233.5; DB 15; Length 186;
Best Local Similarity 33.3%; Pred. No. 9.6e-18;
Matches 61; Conservative 37; Mismatches 72; Indels 13; Gaps 4;

Qy      31 DLEVVLPHGIIVDRIERLAKDIMKDIGYSDIMVLCVLKGGYKFCADLVEHLKNISRNSD 90
Db      11 DLKSVLITKBEIDAKLAELAAKIDAEYAGKDLLIVGLKGVMMVMDLARALS-----63
Qy      91 RFVSMKVPFIRLKS--RNDQSMGEMQIIGGGDLST--LAGKNFLIVEDVVGTRTKALLS 148
Db      64 --TPVTMDMVAVSSYAGTQSSGVVRII--KDLDTDIKKGKHLIIVEDIISDGLTSLWLS 119
Qy      149 NIEKYKPNMKIVASLLVKTSTSDGRPDYAGFEIPLHFLVWGVYALDINEYFRDLNHNICVI 208
Db      120 NLGSRPASLKVCTLLRKPEAAKVAIDVSEWVGFDIPNEFVICYGLDYAEKYNLPFVGTL 179
Qy      209 NEH 211
Db      180 APH 182

RESULT 14
US-09-189-833B-10
; Sequence 10, Application US/09189833B
; Patent No. US2002006593A1
; GENERAL INFORMATION:
; APPLICANT: Bednarik et al.
; TITLE OF INVENTION: Human Hypoxanthine-(Guanine) Phosphoribosyl Transferase-2
; FILE REFERENCE: PFI38P1DI
; CURRENT APPLICATION NUMBER: US/09/189,833B
; CURRENT FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 08/461,031
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: PCT/US94/11914
; PRIOR FILING DATE: 1994-10-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Trypanosoma brucei
US-09-189-833B-10

Query Match      19.9%; Score 222.5; DB 9; Length 210;
Best Local Similarity 29.3%; Pred. No. 1.9e-16;
Matches 54; Conservative 46; Mismatches 65; Indels 19; Gaps 5;

Qy      35 VLPHGIIVDRIERLAKDIMKDIGYSD-----IMVLCVLKGGYKFCADLVEHLKNI 85
Db      13 VLFTEAELHTRMGRGVAQRIADD--YSNCNLKPLENPLVIVSVLKGFSVFTADMVRIL---67
Qy      86 SRNSDRFVSMKVPFIRLKSRYND--QSMGEMQIIGGGDLSTLAGKNFLIVEDVVGTRTK 144
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Db      68 ---GDFGVPTRVVEFLRASSYGHDTKSCGRVDVVKADG-LCDIRGKHVVLVEDILDALTILR 123
QY      145 ALLSNIKYKPMIKVASILLVKRTSRSDGFRPDYAGFEIPHLFVVGVALDYNEYFRDLNH 204
       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      124 EVDLSLKKSEPAIKTLVAIDKPGGRKIPFTAEYVVADVVPNVVVGGLDYDQSYREVVD 183
QY      205 ICVI 208
       : : :
Db      184 VVIL 187

```

```

RESULT 15
US-09-902-705-10
; Sequence 10, Application US/09902705
; Patent No. US20020081695A1
; GENERAL INFORMATION:
; APPLICANT: Bednarik et al.
; TITLE OF INVENTION: Human Hypoxanthine- (Guanine) Phosphoribosyl Transferase-2
; FILE REFERENCE: PFI38P1C1
; CURRENT APPLICATION NUMBER: US/09/902,705
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: US 08/461,031
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: PCT/US94/11914
; PRIOR FILING DATE: 1994-10-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Trypanosoma brucei
US-09-902-705-10

```

```

Query Match      19.9%; Score 222.5; DB 9; Length 210;
Best Local Similarity 29.3%; Pred. No. 1.9e-16;
Matches 54; Conservative 46; Mismatches 65; Indels 19; Gaps 5;

QY      35 VLPHGIIVDRIERLAKDIMGYSD-----IMVLCVLKGGYKFCADLVEHLKNI 85
Db      13 VLFTAEHLTRMRGVAQRIADD--YSCNCLKPLENPLVIVSVLKGFSVFTADMVRIL--- 67

QY      86 SRNSDRFVSMKYDFIRLKSRYND-QSMGEMQIIGGGDLSTLAGKNFLIVEDVVGRTMK 144
Db      68 ---GDFGVPTRVVEFLRASSYGHDTKSCGRVDVVKADG-LCDIRGKHVVLVEDILDALTILR 123

QY      145 ALLSNIKYKPMIKVASILLVKRTSRSDGFRPDYAGFEIPHLFVVGVALDYNEYFRDLNH 204
Db      124 EVDLSLKKSEPAIKTLVAIDKPGGRKIPFTAEYVVADVVPNVVVGGLDYDQSYREVVD 183

QY      205 ICVI 208
       : : :
Db      184 VVIL 187

```

Search completed: November 13, 2003, 15:11:49  
Job time : 31 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 13, 2003, 15:03:26 ; Search time 20 Seconds  
(without alignments)  
1019.388 Million cell updates/sec

Title: US-09-902-705-2  
Perfect score: 1116  
Sequence: 1 MATRSPGVIMDDWPGYDLN.....LDYNEFRDLNHCIVINEHG 212  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues  
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 76:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	786	70.4	218	2 S43043	hypoxanthine (guan
2	783	70.2	214	2 149758	hypoxanthine phosp
3	779	69.8	218	1 RTHUG	hypoxanthine phosp
4	779	69.8	218	2 S21474	hypoxanthine phosp
5	777	69.6	218	1 RTMSG	hypoxanthine phosp
6	776	69.5	218	1 RTHYG	hypoxanthine phosp
7	768	68.8	218	2 I51842	hypoxanthine phosp
8	768	68.8	218	2 S18140	hypoxanthine phosp
9	498.5	44.7	285	2 S09614	hypoxanthine phosp
10	485	43.5	284	2 S04278	hypoxanthine phosp
11	447.5	40.1	231	2 S06601	hypoxanthine phosp
12	446.5	40.0	231	2 S06315	hypoxanthine phosp
13	445.5	39.9	231	2 JN0085	hypoxanthine phosp
14	265.5	23.8	180	2 S66098	hypoxanthine phosp
15	265.5	23.8	180	2 G86814	hypothetical prote
16	261	23.4	183	2 S30100	hypoxanthine phosp
17	261	23.4	183	2 D86627	hypothetical prote
18	257.5	23.1	178	2 H97293	hypoxanthine-guani
19	255	22.8	178	2 A70349	hypoxanthine-guani
20	254.5	22.8	648	2 AD1464	fusion protein, N-
21	250.5	22.4	648	2 AD1102	hypoxanthine-guani
22	247.5	22.2	180	2 D95001	hypoxanthine-guani
23	247.5	22.2	180	2 C97873	hypoxanthine phosp
24	244.5	21.9	175	2 T43437	hypoxanthine phosp
25	239.5	21.5	179	2 G89817	hypothetical prote
26	235.5	21.1	187	2 T36331	probable hypoxanth
27	232.5	20.8	179	2 D83660	hypoxanthine-guani
28	229	20.5	171	2 H72405	hypoxanthine phosp
29	227.5	20.4	216	2 A70561	probable hpt prote

30	223.5	20.0	213	2 F86935	probable hypoxanth
31	222.5	19.9	210	2 S41631	hypoxanthine phosp
32	221	19.8	177	2 E82306	hypoxanthine phosp
33	218	19.5	176	2 S10993	hypoxanthine phosp
34	216.5	19.4	182	2 A90645	hypoxanthine phosp
35	216.5	19.4	182	2 A85496	hypoxanthine phosp
36	216.5	19.4	182	2 S45202	hypoxanthine phosp
37	209	18.7	182	2 S19720	hypoxanthine phosp
38	208.5	18.4	176	2 A75404	hypoxanthine-guani
39	205	18.4	180	2 AB3000	hypoxanthine phosp
40	205	18.4	180	2 G98283	hypoxanthine phosp
41	200	17.9	206	2 C82934	hypoxanthine-guani
42	198.5	17.8	178	2 AB0414	hypoxanthine phosp
43	197.5	17.7	178	2 AH0523	hypoxanthine phosp
44	197	17.7	193	2 G90580	hypothetical prote
45	189	16.9	179	2 D64168	hypoxanthine phosp

ALIGNMENTS

RESULT 1

S43043  
hypoxanthine (guanine) phosphoribosyltransferase - long-tailed hamster  
C;Species: Cricetus longicaudatus (long-tailed hamster)  
C;Date: 07-Sep-1994 #sequence\_revision 26-May-1995 #text\_change 18-Jun-1999  
C;Accession: S43043  
R;Wei, S.J.C.; Chang, R.L.; Bhachech, N.; Cui, X.X.; Merkier, K.A.; Wong, C.Q.; Hennig, Cancer Res. 53, 3294-3301, 1993  
A;Title: Dose-dependent differences in the profile of mutations induced by (+)-7R,8S-di-horibosyltransferase gene in chinese hamster V-79 cells.  
A;Reference number: S43043; MUID:93313862; PMID:8324741  
A;Accession: S43043  
A;Status: preliminary; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-218 <WEI>  
A;Cross-references: EMBL:X59652; NID:g461343; PIDN:CAA42198.1; PID:g461344  
C;Superfamily: hypoxanthine phosphoribosyltransferase

Query Match		70.4%	Score 786;	DB 2;	Length 218;
Best Local Similarity		69.3%	Pred. No. 3.1e-59;		
Matches 147;		Conservative	30;	Mismatches 35;	Indels 0; Gaps 0;
Qy	1	MATRSPGVIMDDWPGYDLNLFYPOHYGDLVLPHPHGIIVDRIERLAKIMKIDIGYS	60		
Db	1	MATRSPSWISDDPEGYDLDFCIPNHYEDELKVFIPHGVIIMDRTERLARDVNKMGGH	60		
Qy	61	DIIVLCVLKGGYKFCADLVEHLKNISSNSDRFVSMKYDFIRLKSRYNDQSGEMQIICGG	120		
Db	61	HIIVLCVLKGGYKFCADLVEHLKNISSNSDRFVSMKYDFIRLKSRYNDQSGEMQIICGG	120		
Qy	121	DLSTLAGKNFLIVEDVVGTRTKALLSNIEKYKPNMKIVASLLVKTTSRSDGFRPDYAG	180		
Db	121	DLSTLTGKNVLIVEDIIDTGTQTLTLVLRKYNPKVKVVASLLVKTTSRSGVRPDEVG	180		
Qy	181	FEIPLFPVGYALDYNEFRDLNHCIVINEHG	212		
Db	181	FEIPDKFVGYALDYNEFRDLNHCIVISETG	212		

RESULT 2

I49758  
hypoxanthine phosphoribosyltransferase (BC 2.4.2.8) - western wild mouse (fragment)  
C;Species: Mus spretus (western wild mouse)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 18-Jun-1999  
C;Accession: I49758  
R;Johnson, G.G.; Kronert, W.A.; Bernstein, S.I.; Smith, K.D. J. Biol. Chem. 263, 9079-9082, 1988  
A;Title: Altered turnover of allelic variants of hypoxanthine phosphoribosyltransferase  
A;Reference number: I49758; MUID:88243783; PMID:3379061  
A;Accession: I49758  
A;Status: preliminary; translated from GB/EMBL/DBD  
A;Molecule type: mRNA





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Db      1 MATRSPGVVISDDEFGYDLDFCIPNHVYAEADLERVFIPLHGLIMDRTERLARDVMKEMGGH 60
QY      61 DIMVLVLKGGYKFCADLVEHLKNTSRNSDRFVSMKVDFIRLKSRYNDQSMGEMQIIGG 120
Db      61 HIVALCVLKGKGFADLLDYIKALNRNSDRSIPMTVDFIRLKSRYNDQSGDGIKVIIGD 120
QY      121 DLSTLAGKNFLIVEDVVGTRTKALLSNIKYKPMIKVASLLVKRTSRSDGFRPDYAG 180
Db      121 DLSTLTGKNVLIVEDIIDTGKTMQTLTLVLRQYNPKMKVVASLLVKRTSRSGVYRPFDFVG 180
QY      181 FEIPLFVVGVALDYNEFRDLNHLHCIVINEHG 212
Db      181 FEIPDKFVVGVALDYNEFRDLNHLVCVISETG 212

RESULT 4
S21474
hypoxanthine phosphoribosyltransferase (EC 2.4.2.8) - long-tailed hamster
N:Alternate names: hypoxanthine guanine phosphoribosyltransferase
C:Species: Crictetus longicaudatus (long-tailed hamster)
C:Date: 22-Nov-1993 #sequence revision 10-Nov-1995 #text_change 18-Jun-1999
C:Accession: S21474
R:Rossiter, F.; Muzny, M.; Caskey, T.; Fox, M.
A:Description: A Chinese hamster HPRT point mutation reverts to the wild-type sequence.
A:Reference number: S21474
A:Accession: S21474
A:Molecule type: mRNA
A:Residues: 1-218 <ROS>
A:Cross-references: EMBL:X17656; NID:g49514; PIDN:CAA35648.1; PID:g49515
C:Superfamily: hypoxanthine phosphoribosyltransferase
C:Keywords: glycosyltransferase; pentosyltransferase

Query Match      69.8%; Score 779; DB 2; Length 218;
Best Local Similarity 68.9%; Pred. No. 1.2e-58;
Matches 146; Conservative 30; Mismatches 36; Indels 0; Gaps 0;

QY      1 MATRSPGVVIMDDWPGYDLNLTYPQHYVGDLEYVLPHGIIVDRIERLAKDIMKDIGYS 60
Db      1 MATRSPSVVISDDEFGYDLDFCIPNHVYAEADLERVFIPLHGLIMDRTERLARDVMKEMGGH 60
QY      61 DIMVLVLKGGYKFCADLVEHLKNTSRNSDRFVSMKVDFIRLKSRYNDQSMGEMQIIGG 120
Db      61 HIVALCVLKGKGFADLLDYIKALNRNSDRSIPMTVDFIRLKSRYNDQSGDGIKVIIGD 120
QY      121 DLSTLAGKNFLIVEDVVGTRTKALLSNIKYKPMIKVASLLVKRTSRSDGFRPDYAG 180
Db      121 DLSTLTGKNVLIVEDIIDTGKTMQTLTLVLRQYNPKMKVVASLLVKRTSRSGVYRPFDFVG 180
QY      181 FEIPLFVVGVALDYNEFRDLNHLHCIVINEHG 212
Db      181 FEIPDKFVVGVALDYNEFRDLNHLVCVISETG 212

RESULT 5
RTMSG
hypoxanthine phosphoribosyltransferase (EC 2.4.2.8) - mouse
N:Alternate names: hypoxanthine-guanine phosphoribosyltransferase
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1989 #sequence revision 09-Aug-1997 #text_change 11-Jun-1999
C:Accession: I49756; A26218; A00579
R:Melton, D.W.; Konecki, D.S.; Brennan, J.; Caskey, C.T.
Proc. Natl. Acad. Sci. U.S.A. 84, 2147-2151, 1984
A:Title: Structure, expression, and mutation of the hypoxanthine phosphoribosyltransferase
A:Reference number: I49756; MUID:84193967; PMID:6326107
A:Accession: I49756
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-218 <RES>
A:Cross-references: GB:K01515; NID:g193994; PIDN:AAA96271.1; PID:g387206
R:Konecki, D.S.; Brennan, J.; Fuscoe, J.C.; Caskey, C.T.; Chinault, A.C.
Nucleic Acids Res. 10, 6763-6775, 1982

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A:Title: Hypoxanthine-guanine phosphoribosyltransferase genes of mouse and Chinese hams
A:Reference number: A93446; MUID:83090437; PMID:6294614
A:Accession: A26218
A:Molecule type: mRNA
A:Residues: 2-200, 'N', 202-218 <KON>
A:Cross-references: GB:J00423; NID:g193984; PIDN:AAA96232.1; PID:g309315
A:Note: initiator Met not shown
A:Note: this variant protein has enzymatic activity and its sequence is expected to be
line having no enzymatic activity
C:Genetics:
A:Introns: 9/3; 45/2; 106/3; 128/3; 134/3; 162/2; 178/1; 203/3
C:Superfamily: hypoxanthine phosphoribosyltransferase
C:Keywords: glycosyltransferase; pentosyltransferase; salvage pathway

Query Match      69.6%; Score 777; DB 1; Length 218;
Best Local Similarity 68.4%; Pred. No. 1.8e-58;
Matches 145; Conservative 31; Mismatches 36; Indels 0; Gaps 0;

QY      1 MATRSPGVVIMDDWPGYDLNLTYPQHYVGDLEYVLPHGIIVDRIERLAKDIMKDIGYS 60
Db      1 MPTRSPSVVISDDEFGYDLDFCIPNHVYAEADLERVFIPLHGLIMDRTERLARDVMKEMGGH 60
QY      61 DIMVLVLKGGYKFCADLVEHLKNTSRNSDRFVSMKVDFIRLKSRYNDQSMGEMQIIGG 120
Db      61 HIVALCVLKGKGFADLLDYIKALNRNSDRSIPMTVDFIRLKSRYNDQSGDGIKVIIGD 120
QY      121 DLSTLAGKNFLIVEDVVGTRTKALLSNIKYKPMIKVASLLVKRTSRSDGFRPDYAG 180
Db      121 DLSTLTGKNVLIVEDIIDTGKTMQTLTLVLRQYNPKMKVVASLLVKRTSRSGVYRPFDFVG 180
QY      181 FEIPLFVVGVALDYNEFRDLNHLHCIVINEHG 212
Db      181 FEIPDKFVVGVALDYNEFRDLNHLVCVISETG 212

RESULT 6
RTHYG
hypoxanthine phosphoribosyltransferase (EC 2.4.2.8) - Chinese hamster
N:Alternate names: hypoxanthine-guanine phosphoribosyltransferase
C:Species: Crictetus griseus (Chinese hamster)
C:Date: 31-Dec-1989 #sequence revision 12-Apr-1996 #text_change 01-Dec-2000
C:Accession: S14402; A26219; J59003; A00579
R:Rossiter, B.J.F.; Fuscoe, J.C.; Muzny, D.M.; Fox, M.; Caskey, C.T.
Genomics 9, 247-256, 1991
A:Title: The Chinese hamster HPRT gene: restriction map, sequence analysis, and multipl
A:Reference number: S14402; MUID:91169526; PMID:2004774
A:Accession: S14402
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-218 <ROS>
A:Cross-references: EMBL:X53073; NID:g49505; PIDN:CAA37247.1; PID:g817936
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1990
R:Konecki, D.S.; Brennan, J.; Fuscoe, J.C.; Caskey, C.T.; Chinault, A.C.
Nucleic Acids Res. 10, 6763-6775, 1982
A:Title: Hypoxanthine-guanine phosphoribosyltransferase genes of mouse and Chinese hams
A:Reference number: A93446; MUID:83090437; PMID:6294614
A:Accession: A26219
A:Molecule type: mRNA
A:Residues: 2-218 <KON>
A:Cross-references: GB:J00060; NID:g191112; PIDN:AAA36990.1; PID:g304515
A:Note: initiator Met not shown
A:Note: this variant protein has enzymatic activity and its sequence is expected to be
line having no enzymatic activity
R:Fuscoe, J.C.; Zimmerman, L.J.; Pekete, A.; Setzer, R.W.; Rossiter, B.J.
Mutat. Res. 269, 171-183, 1992
A:Title: Analysis of X-ray-induced HPRT mutations in CHO cells: insertion and deletions
A:Reference number: I58003; MUID:93024555; PMID:1383700
A:Accession: I58003
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 32-44 <RES>
A:Cross-references: GB:S46270; NID:g257049
C:Genetics:

```



Query Match 44.7%; Score 498.5; DB 2; Length 285;  
Best Local Similarity 48.6%; Pred. No. 9e-35;  
Matches 101; Conservative 40; Mismatches 64; Indels 3; Gaps 1;

QY 8 VVIMDDPFGVDLNLFTYPQHYYGDEVLVPLPHGIIVDRIERLAKDIM--KDITYSDIMV 64  
Db :  
65 VVIEDSRGPPTTEYFCTSPRYDECLDVLIPNGMIKORLEKMGMDIIVDYEACNATSIITL 124  
QY :  
65 LCVLKGGYKFCADLVEHLKNISNRDSRFVSMKVDFIRLKSRYRNDQSGEMQIIIGGGDLST 124  
Db :  
125 MCVLKGGFKFLADLVGLERTVRARGIVLPMSVEFVRVKSVYVNDVSIHEPILTGLGDPS 184  
QY :  
125 LAGKNFLIVEDVVGTRTKMALLSNIEKYKPNMKIVASLLVKRTSDDGRPDYAGFEIP 184  
Db :  
185 YKDKNVLVVEDIIDTGKTITKLISHLSLSTSKVKVASLLVKRTSPRDYRPDPVGFPEVP 244  
QY :  
185 HLFVVGVALDYNEXFRDLNHICVINEHG 212  
Db :  
245 NRVVVGVALDYNDFRLDHHICVINEVG 272

RESULT 10  
S04278  
hypoxanthine phosphoribosyltransferase (EC 2.4.2.8) - fluke (Schistosoma mansoni)  
N;Alternate names: hypoxanthine-guanine phosphoribosyltransferase  
C;Species: Schistosoma mansoni  
C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 20-Jun-2000  
C;Accession: S04278; S01201  
R;Craig, S.P.; Muralidhar, M.G.; McKerrow, J.H.; Wang, C.C.  
submitted to the EMBL Data Library, November 1988  
A;Reference number: S04278  
A;Accession: S04278  
A;Molecule type: DNA  
A;Residues: 1-284 <CRA>  
A;Cross-references: EMBL:X13531; NID:g10181; PIDN:CAA31885.1; PID:g1197381  
R;Craig III, S.P.; McKerrow, J.H.; Newport, G.R.; Wang, C.C.  
Nucleic Acids Res. 16, 7087-7101, 1988  
A;Title: Analysis of cDNA encoding the hypoxanthine-guanine phosphoribosyltransferase (H  
A;Reference number: S01201; MUID:88303331; PMID:3136439  
A;Accession: S01201  
A;Molecule type: mRNA  
A;Residues: 1-231 <CRA2>  
A;Cross-references: EMBL:X07883  
C;Genetics:  
A;Introns: 66/3; 102/3; 166/3; 188/3; 221/3; 237/3; 262/3  
C;Superfamily: hypoxanthine phosphoribosyltransferase  
C;Keywords: glycosyltransferase; pentosyltransferase; salvage pathway

Query Match 43.5%; Score 485; DB 2; Length 284;  
Best Local Similarity 48.6%; Pred. No. 1.2e-33;  
Matches 101; Conservative 39; Mismatches 64; Indels 4; Gaps 2;

QY 8 VVIMDDPFGVDLNLFTYPQHYYGDEVLVPLPHGIIVDRIERLAKDIM--KDITYSDIMV 64  
Db :  
65 VVIEDSRGPPTTEYFCTSPRYDECLDVLIPNGMIKORLEKMGMDIIVDYEACNATSIITL 124  
QY :  
65 LCVLKGGYKFCADLVEHLKNISNRDSRFVSMKVDFIRLKSRYRNDQSGEMQIIIGGGDLST 124  
Db :  
125 MCVLKGGFKFLADLVGLERTVRARGIVLPMSVEFVRVKSVYVNDVSIHEPILTGLGDPS 184  
QY :  
125 LAGKNFLIVEDVVGTRTKMALLSNIEKYKPNMKIVASLLVKRTSDDGRPDYAGFEIP 184  
Db :  
185 YKDKNVLVVEDIIDTGKTITKLISHLSLSTSKVKVASLLVKRTSPRDYRPDPVGFPEVP 243  
QY :  
185 HLFVVGVALDYNEXFRDLNHICVINEHG 212  
Db :  
244 NRVVVGVALDYNDFRLDHHICVINEVG 271

RESULT 11  
S06601  
hypoxanthine phosphoribosyltransferase (EC 2.4.2.8) - malaria parasite (Plasmodium falci





GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: November 13, 2003, 14:59:46 ; Search time 17 seconds  
(without alignments)  
586.451 Million cell updates/sec

Title: US-09-902-705-2

Perfect score: 1116

Sequence: 1 MATRSPGVVIMDFGDLN.....LDYNEVFRDLNHCIVINEHG 212

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	778	69.7	213	1 HPRT_MUSSP	Q64531 mus spretus
2	774	69.4	217	1 HPRT_HUMAN	P00492 homo sapien
3	773	69.3	217	1 HPRT_MOUSE	P00493 mus musculus
4	771	69.1	217	1 HPRT_CRIGR	P00494 cricetus
5	771	69.1	217	1 HPRT_MERUN	P47959 meriones un
6	768	68.8	218	1 HPRT_RAT	P27605 rattus norv
7	753	67.5	218	1 HPRT_CHICK	Q9w719 gallus gall
8	485	43.5	284	1 HPRT_SCHMA	P09383 schistosoma
9	447.5	40.1	231	1 HGXR_PLAFK	P20035 plasmodium
10	446.5	40.0	231	1 HGXR_PLAFK	P07833 plasmodium
11	346	31.0	230	1 HGXR_TOXGO	Q26997 toxoplasma
12	265.5	23.8	180	1 HPRT_BACSU	P37472 bacillus su
13	261	23.4	183	1 HPRT_LACLA	Q02522 lactococcus
14	255	22.8	178	1 HPRT_AQUAE	Q66821 aquifex aeo
15	234.5	21.0	183	1 HGXR_TRIFO	P51900 tritrichomo
16	232.5	20.8	203	1 HPRT_MYCAV	P96794 mycobacteri
17	227.5	20.4	202	1 HPRT_MYCTU	Q06383 mycobacteri
18	223.5	20.0	203	1 HPRT_MYCLE	Q69537 mycobacteri
19	222.5	19.9	210	1 HPRT_TRYBB	Q07010 trypanosoma
20	219	19.6	208	1 HPRT_CRYFA	Q27541 crithidia f
21	218.5	19.6	211	1 HPRT_LEIDH	P43152 leishmania
22	218.5	19.5	176	1 HPRT_VIBHA	P18134 vibrio harv
23	216.5	19.4	178	1 HPRT_ECOLI	P36766 escherichia
24	214.5	19.2	177	1 HPRT_BUCAP	Q8K908 buchnera ap
25	209	18.7	182	1 HPRT_RHOCA	P37171 rhodobacter
26	204.5	18.3	178	1 HPRT_SALTY	Q33799 salmonella
27	192	17.2	178	1 HPRT_BUCAI	P57291 buchnera ap
28	189	16.9	179	1 HPRT_HABIN	P45078 haemophilus
29	160.5	14.4	175	1 HPRT_MYCPN	P75119 mycoplasma
30	139.5	12.5	175	1 HPRT_MYCGE	P47696 mycoplasma
31	137	12.3	180	1 PYRR_BACHD	Q8K9W4 bacillus ha
32	126.5	11.3	178	1 PYRR_ENTFA	Q52707 enterococcu
33	122.5	11.0	173	1 PYRR_STRPN	Q97qel streptococc

34	121	10.8	178	1 PYRR_CLOAB	Q97ha0 clostridium
35	120.5	10.8	178	1 PYRR_THETN	Q8r9r3 thermoanaer
36	119	10.7	178	1 PYRR_CLOPE	Q8xjb2 clostridium
37	117	10.5	192	1 PYRR_CORGL	P59011 corynebacte
38	116.5	10.4	180	1 PYRR_ANASL	Q8yvv8 anabaena sp
39	116	10.4	180	1 PYRR_LACPL	P71479 lactobacilli
40	116	10.4	180	1 PYRR_STRCO	Q9kxri streptomyce
41	115.5	10.3	178	1 PYRR_SYNY3	Q85758 synechocyst
42	114.5	10.3	173	1 PYRR_STRP3	Q8k7y5 streptococc
43	114.5	10.3	173	1 PYRR_STRPY	Q9a0d0 streptococc
44	113.5	10.2	179	1 PYRR_HASIN	P44722 haemophilus
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## ALIGNMENTS

RESULT 1  
HPRT\_MUSSP  
ID HPRT\_MUSSP STANDARD; PRT; 213 AA.  
AC Q64531;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8) (HGPR)  
DE (HGPRase) (HPRT A) (Fragment).  
GN HPRT.  
OS Mus spretus (Western wild mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_taxonomy=10096;  
RN [1]  
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RC TISSUE=Brain;  
RX MEDLINE=88243783; PubMed=3379061;  
RA Johnson G.G., Kronert W.A., Bernstein S.I., Chapman V.M., Smith K.D.;  
RT "Altered turnover of allelic variants of hypoxanthine  
phosphoribosyltransferase is associated with N-terminal amino acid  
sequence variation.";  
RL J. Biol. Chem. 263:9079-9082(1988).  
CC -!- CATALYTIC ACTIVITY: IMP + diphosphate = hypoxanthine + 5-phospho-  
alpha-D-ribose 1-diphosphate.  
CC -!- CATALYTIC ACTIVITY: GMP + diphosphate = guanine + 5-phospho-  
alpha-D-ribose 1-diphosphate.  
CC -!- PATHWAY: Purine salvage.  
CC -!- SUBUNIT: Homotrimer (By similarity).  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -!- SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE  
PHOSPHORIBOSYLTRANSFERASE FAMILY.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC EMBL; M20011; AAA96234.1; -;  
DR PIR; I49758; I49758.  
DR HSSP; P00492; 1B2Y.  
DR MGD; MGI:96217; Hprt.  
DR InterPro; IPR005904; Hxn phspho trans.  
DR InterPro; IPR002375; PY\_PY\_ID\_transf.  
DR InterPro; IPR000936; PRTtransferase.  
DR Pfam; PF00156; Pribosyltran; 1.  
DR TIGRFAMs; TIGR01203; HGPRase; 1.  
DR PROSITE; P500103; PUR PYR PR TRANSFER; 1.  
KW Transferase; Glycosyltransferase; Purine salvage; Magnesium;  
KW Acetylation.  
FT INIT\_MET 0 0  
FT MOD\_RES 1 1 ACETYLATION (PROBABLE).  
FT METAL 133 133 MAGNESIUM (BY SIMILARITY).

FT METAL 134 134 MAGNESIUM (BY SIMILARITY).  
 FT NON TER 213 213  
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 Best Local Similarity 68.7%; Pred. No. 5.6e-58;  
 Matches 145; Conservative 31; Mismatches 35; Indels 0; Gaps 0;  
 QY 2 ATRSPGVIMDDWPGYDLNLFYQHYGDELYVLIPIPHGIIIVDRIERLAKDWMKQIGYSD 61  
 DB 1 ATRSPSVISDEPGYDLNLFYQHYGDELYVLIPIPHGIIIVDRIERLAKDWMKQIGYSD 60  
 QY 62 IMVLCVLKGGYKFCADLVHKLKNISSNRDRFVSMKVDFIRLKSYNRNDQSGMEQIIGGD 121  
 DB 61 IVALCVLKGKGYKFCADLVHKLKNISSNRDRFVSMKVDFIRLKSYNRNDQSGMEQIIGGD 120  
 QY 122 LSTLAKGNFLIYEDVVGTGRTKALLSNTKPKVPMIKVASILLVKTSSDGRPDYAGF 181  
 DB 121 LSTLTKGNVLIYEDVVGTGRTKALLSNTKPKVPMIKVASILLVKTSSDGRPDYAGF 180  
 QY 182 EIPHLFVVGVALDYNEYFRDLNHLHCIVNEHG 212  
 DB 181 EIPDKFVVGVALDYNEYFRDLNHLHCIVNEHG 211  
 RESULT 2  
 HPRT HUMAN STANDARD; PRT; 217 AA.  
 AC P00492;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8) (HGPR)  
 DE (HGPRase).  
 GN HPRT1 OR HPRT.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=82265815; PubMed=7107641;  
 RA Wilson J.M., Tarr G.E., Mahoney W.C., Kelley W.N.;  
 RT "Human hypoxanthine-guanine phosphoribosyltransferase. Complete amino  
 acid sequence of the erythrocyte enzyme.";  
 RL J. Biol. Chem. 257:10978-10985(1982).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=83169681; PubMed=6300847;  
 RA Jolly D.J., Okayama H., Berg P., Esty A.C., Filipula D., Bohlen P.,  
 RA Johnson G.G., Shively J.E., Hunkapiller T., Friedmann T.;  
 RT "Isolation and characterization of a full-length expressible cDNA for  
 human hypoxanthine phosphoribosyl transferase.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 80:477-481(1983).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90256168; PubMed=2341149;  
 RA Edwards A., Voss H., Rice P., Civitello A., Stegemann J.,  
 RA Schwager C., Zimmermann J., Erle H., Caskey C.T., Ansorge W.;  
 RT "Automated DNA sequencing of the human HPRT locus.";  
 RL Genomics 6:593-608(1990).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [5]  
 RP SEQUENCE OF 1-8 FROM N.A.  
 RX MEDLINE=87064322; PubMed=3023844;  
 RA Patel P.I., Framson P.E., Caskey C.T., Chinault A.C.;  
 RT "Fine structure of the human hypoxanthine phosphoribosyltransferase  
 gene.";  
 RL Mol. Cell. Biol. 6:393-403(1986).  
 RN [6]  
 RP X-RAY CRYSTALLOGRAPHY (2.45 ANGSTROMS).  
 RX MEDLINE=94320143; PubMed=8044844;  
 RA Bads J.C., Scapin G., Xu Y., Grubmeyer C., Sacchettini J.C.;  
 RT "The crystal structure of human hypoxanthine-guanine  
 phosphoribosyltransferase with bound GMP.";  
 RL Cell 78:325-344(1994).  
 RN [7]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
 RX MEDLINE=99287111; PubMed=10360366;  
 RA Shi W., Li C.M., Tyler P.C., Furneaux R.H., Grubmeyer C.,  
 RA Schramm V.L., Almo S.C.;  
 RT "The 2.0 A structure of human hypoxanthine-guanine  
 phosphoribosyltransferase in complex with a transition-state analog  
 inhibitor.";  
 RL Nat. Struct. Biol. 6:588-593(1999).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).  
 RX MEDLINE=99268335; PubMed=10338013;  
 RA Balendiran G.K., Molina J.A., Xu Y., Torres-Martinez J., Stevens R.,  
 RA Focia P.J., Eakin A.E., Sacchettini J.C., Craig S.P. III;  
 RT "Ternary complex structure of human HGPRTase, PRPP, Mg2+, and the  
 inhibitor HPP reveals the involvement of the flexible loop in  
 substrate binding.";  
 RL Protein Sci. 8:1023-1031(1999).  
 RN [9]  
 RP REVIEW ON VARIANTS.  
 RX MEDLINE=93138599; PubMed=1487231;  
 RA Sculley D.G., Dawson P.A., Emmerson B.T., Gordon R.B.;  
 RT "A review of the molecular basis of hypoxanthine-guanine  
 phosphoribosyltransferase (HGPRT) deficiency.";  
 RL Hum. Genet. 90:195-207(1992).  
 RN [10]  
 RP VARIANT TORONTO.  
 RX MEDLINE=83213351; PubMed=6853490;  
 RA Wilson J.M., Kobayashi R., Fox I.H., Kelley W.N.;  
 RT "Human hypoxanthine-guanine phosphoribosyltransferase.";  
 RL J. Biol. Chem. 258:6458-6460(1983).  
 RN [11]  
 RP VARIANT KINSTON.  
 RX MEDLINE=83213940; PubMed=6853716;  
 RA Wilson J.M., Kelley W.N.;  
 RT "Molecular basis of hypoxanthine-guanine phosphoribosyltransferase  
 deficiency in a patient with the Lesch-Nyhan syndrome.";  
 RL J. Clin. Invest. 71:1331-1335(1983).  
 RN [12]  
 RP VARIANT LONDON.  
 RX MEDLINE=83144031; PubMed=6572373;  
 RA Wilson J.M., Tarr G.E., Kelley W.N.;  
 RT "Human hypoxanthine (guanine) phosphoribosyltransferase: an amino  
 acid substitution in a mutant form of the enzyme isolated from a  
 patient with gout.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 80:870-873(1983).  
 RN [13]





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DR EMBL; J00423; AA96232.1; -.
DR EMBL; K01515; AAA96271.1; -.
DR EMBL; K01507; AAA96271.1; JOINED.
DR EMBL; K01508; AAA96271.1; JOINED.
DR EMBL; K01509; AAA96271.1; JOINED.
DR EMBL; K01510; AAA96271.1; JOINED.
DR EMBL; K01511; AAA96271.1; JOINED.
DR EMBL; K01512; AAA96271.1; JOINED.
DR EMBL; K01513; AAA96271.1; JOINED.
DR EMBL; K01514; AAA96271.1; JOINED.
DR PIR; I49756; RTMSG.
DR HSP; P00492; LHMP.
DR MGD; MGI.96217; Hprt.
DR InterPro; IPR005904; Hxn phspho trans.
DR InterPro; IPR002375; Pr/PY_rP_transf.
DR InterPro; IPR000836; Prtransferase.
DR Pfam; PF00156; Priboyltran; 1.
DR TIGRfams; TIGR01203; HGPRTase; 1.
DR PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.
KW Transferase; Glycosyltransferase; Purine salvage; Magnesium.
FT INIT_MET 0
FT METAL 133 133 MAGNESIUM (BY SIMILARITY).
FT METAL 134 134 MAGNESIUM (BY SIMILARITY).
FT CONFLICT 200 200 D -> N (IN REF. 1).
SQ SEQUENCE 217 AA; 24439 MW; A21CCD4DB64693B5 CRC64;
Query Match 69.3%; Score 773; DB 1; Length 217;
Best Local Similarity 68.6%; Pred. No. 1.5e-57;
Matches 144; Conservative 31; Mismatches 35; Indels 0; Gaps 0;
Qy 3 TRSPGVIMDDPFGYDLNLFYTPQHYGDLVYLPHGIIIVDRIBRLAKDIMKDIGSDI 62
Db 2 TRSFVVISDEPGYDLDFCIPNHYAEDLEKVFIPHGLINDRTERLARDVMKGGHHI 61
Qy 63 MVLCLVKGKGYKFCADLVEHLKNIISNRSDRFVSMKVDFIRLKSRYNDQSMGEMQIIGGDL 122
Db 62 VALCLVKGKGYKFCADLVEHLKNIISNRSDRFVSMKVDFIRLKSRYNDQSGTGDIKVIIGGDL 121
Qy 123 STLAKGNFLIVEDVGTGTMTKALLSNIEKYKPNMKIVASLLVKRTSRSDGPRPDYAGFE 182
Db 122 STLTGKNVLIVEDIIDTGKTMQTLLSLVKQSPKMKVVASLLVKRTSRSGYRDFVGF 181
Qy 183 IPHLFVVGVALDYNEFYFDLNHCIVINEHG 212
Db 182 IPDKFVVGVALDYNEFYFDLNHCIVINEHG 211

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RESULT 4  
 ID HPRT\_CRIGR STANDARD; PRT; 217 AA.  
 AC P00494;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8) (HGPRT)  
 GN HGPRTase).

OS Cricetus griseus (Chinese hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Cricetulus.  
 OC NCBI\_TaxID=10029;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9116526; PubMed=2004774;  
 RA Rossiter B.J.F., Fuscoe J.C., Muzny D.M., Fox M., Caskey C.T.;  
 FT "The Chinese hamster HPRT gene: restriction map, sequence analysis,  
 RT and multiplex PCR deletion screen."

```

RL Genomics 9:247-256(1991).
RN [2]
RX MEDLINE=83090437; PubMed=6294614;
RA Konecki D.S., Brennan J., Fuscoe J.C., Caskey C.T., Chinault A.C.;
RT "Hypoxanthine-guanine phosphoribosyltransferase genes of mouse and
RT Chinese hamster: construction and sequence analysis of cDNA
RT recombinants."
RL Nucleic Acids Res. 10:6763-6775(1982).
CC -!- CATALYTIC ACTIVITY: IMP + diphosphate = hypoxanthine + 5-phospho-
CC alpha-D-ribose 1-diphosphate.
CC -!- CATALYTIC ACTIVITY: GMP + diphosphate = guanine + 5-phospho-
CC alpha-D-ribose 1-diphosphate.
CC -!- PATHWAY: Purine salvage.
CC -!- SUBUNIT: Homotetramer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- MISCELLANEOUS: THE CELL LINES FROM WHICH THIS SEQUENCE WAS CLONED
CC ARE REVERTANTS FROM MUTANTS WITH NO DETECTABLE ENZYME ACTIVITY.
CC THE PHENOTYPIC REVERSIONS ARE THE RESULT OF OVERPRODUCTION OF
CC VARIANT ENZYMES BECAUSE OF GENE AMPLIFICATION. THIS VARIANT
CC SEQUENCE IS EXPECTED TO BE VERY SIMILAR TO THE WILD TYPE.
CC -!- SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE
CC PHOSPHORIBOSYLTRANSFERASE FAMILY.
CC
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DR EMBL; X53073; CAA37247.1; -.
DR EMBL; X53074; CAA37247.1; JOINED.
DR EMBL; X53075; CAA37247.1; JOINED.
DR EMBL; X53076; CAA37247.1; JOINED.
DR EMBL; X53077; CAA37247.1; JOINED.
DR EMBL; X53078; CAA37247.1; JOINED.
DR EMBL; X53079; CAA37247.1; JOINED.
DR EMBL; X53080; CAA37247.1; JOINED.
DR EMBL; J00060; AAA36990.1; -.
DR PIR; S14402; RTHYG.
DR HSP; P00492; LHMP.
DR InterPro; IPR005904; Hxn_phspho_trans.
DR InterPro; IPR002375; Pr/PY_rP_transf.
DR InterPro; IPR000836; Prtransferase.
DR Pfam; PF00156; Priboyltran; 1.
DR TIGRfams; TIGR01203; HGPRTase; 1.
DR PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.
KW Transferase; Glycosyltransferase; Purine salvage; Magnesium.
FT INIT_MET 0
FT METAL 133 133 MAGNESIUM (BY SIMILARITY).
FT METAL 134 134 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 217 AA; 24512 MW; 119A67BF990F88A1 CRC64;
Query Match 69.1%; Score 771; DB 1; Length 217;
Best Local Similarity 68.7%; Pred. No. 2.2e-57;
Matches 145; Conservative 30; Mismatches 36; Indels 0; Gaps 0;
Qy 2 ATRSPGVIMDDPFGYDLNLFYTPQHYGDLVYLPHGIIIVDRIBRLAKDIMKDIGSD 61
Db 1 ATRSPGVISDEPGYDLDFCIPNHYAEDLEKVFIPHGLINDRTERLARDVMKGGHH 60
Qy 62 IMVLCLVKGKGYKFCADLVEHLKNIISNRSDRFVSMKVDFIRLKSRYNDQSMGEMQIIGGDL 121
Db 61 IVALCLVKGKGYKFCADLVEHLKNIISNRSDRFVSMKVDFIRLKSRYNDQSGTGDIKVIIGD 120
Qy 122 LSTLAGNFLIVEDVGTGTMTKALLSNIEKYKPNMKIVASLLVKRTSRSDGPRPDYAGFE 181
Db 121 LSTLTGKNVLIVEDIIDTGKTMQTLLSLVKRYNLKMKVVASLLVKRTSRSGYRDFVGF 180
Qy 182 EIPHLFVVGVALDYNEFYFDLNHCIVINEHG 212

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Db 181 EIPDKFVGVGALDYNEFERDLNHCIVISGTG 211
RESULT 5
HPRT MERUN STANDARD; PRT; 217 AA.
AC P47959;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8) (HGPRPT)
DE (HGPRPTase).
GN HPRT.
OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Meriones.
OC NCBI_TaxID=10047;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=9918980; PubMed=10090010;
RA Mai Z., Horobov D.W., Klei T.R.;
RT "Hypoxanthine phosphoribosyltransferase cDNA in gerbils (Meriones
unquiculatus)".
RL Lab. Anim. Sci. 48:179-183(1998).
CC -1- CATALYTIC ACTIVITY: IMP + diphosphate = hypoxanthine + 5-phospho-
alpha-D-ribose 1-diphosphate.
CC -1- CATALYTIC ACTIVITY: GMP + diphosphate = guanine + 5-phospho-
alpha-D-ribose 1-diphosphate.
CC -1- PATHWAY: Purine salvage.
CC -1- SUBUNIT: Homotetramer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE
PHOSPHORIBOSYLTRANSFERASE FAMILY.
CC
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or send an email to license@isb-sib.ch).
CC
CC EMBL; L37778; AAA65676.1; -.
CC HSSP; P00492; 1BZY.
CC InterPro; IPR005904; Hxn_phospho_trans.
CC InterPro; IPR002375; Pr/py_rp_transf.
CC InterPro; IPR000836; Prtransferase.
CC Pfam; PF00156; Priboyltran; 1.
CC TIGRFAMs; TIGR01203; HGPRPTase; 1.
CC PROSITE; PS00103; PUR_PIR_PR_TRANSFER; 1.
CC Transferase; Glycosyltransferase; Purine salvage; Magnesium.
FT INIT_MET 0
FT METAL 133 133 MAGNESIUM (BY SIMILARITY).
FT METAL 134 134 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 217 AA; 24407 MW; 68DC5D9397A8144C CRC64;
Query Match 69.1%; Score 771; DB 1; Length 217;
Best Local Similarity 67.3%; Pred. No. 2.2e-57;
Matches 142; Conservative 34; Mismatches 35; Indels 0; Gaps 0;
QY 2 ATRSPGVIMDWPQYDLNLTFTYQHYGDIYVLLPHGIIVDRIERLAKDIMKDIGYSD 61
DB 1 ATRSPSIVIGDEFGYDLDLFCIPKHYAEDLEKVFIPHGLIMDRTERLARDVMKMGHH 60
QY 62 IMVLVLKGGYKFCADLVHEHAKNISRSNDRFVSMKVFIRLKSYPNDSQMGEMQIIIGGD 121
DB 1 IVALCVLGGYKFFADLLDYIKSLNRNTRDPSIPMTVDIFIRLKSVCNDQSTGDIKVIIGDD 120
QY 122 LSTLAGKNFLVEDVVGTRMTKALLSNIEKYKPNMKVASLAVKRTSRSDGFRPDYAGF 181
DB 121 LSALTGRKNVLVEDIIDTGTQNTLLSLVQKISPMKVASLLVTRTPRSVGRAPDFVG 180

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QY 182 EIPHLFVVGVALDYNEFERDLNHCIVINEHG 212
DB 181 EIPDKFVGVGALDYNEFERDLNHCIVISEG 211
RESULT 6
HPRT RAT STANDARD; PRT; 218 AA.
AC P27605; Q62926;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8) (HGPRPT)
DE (HGPRPTase).
GN HPRT.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92147115; PubMed=1783384;
RA Chiaverotti T.A., Battula N., Monnat R.J. Jr.;
RT "Rat hypoxanthine phosphoribosyltransferase cDNA cloning and sequence
analysis."
RL Genomics 11:1158-1160(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92142869; PubMed=1781355;
RA Chiaverotti T.A., Battula N., Monnat R.J. Jr.;
RT "Rat hypoxanthine phosphoribosyltransferase cDNA cloning and sequence
analysis."
RL Adv. Exp. Med. Biol. 309B:117-120(1991).
RN [3]
RP SEQUENCE FROM N.A.
RA Jansen J., Vrieling H., van Zeeland A., Mohn G.;
RL Submitted (NOV-1991) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Fischer 344; TISSUE=Spleen;
RA Chen T., Mittelsaetd R.A., Heflich R.H.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: IMP + diphosphate = hypoxanthine + 5-phospho-
alpha-D-ribose 1-diphosphate.
CC -1- CATALYTIC ACTIVITY: GMP + diphosphate = guanine + 5-phospho-
alpha-D-ribose 1-diphosphate.
CC -1- PATHWAY: Purine salvage.
CC -1- SUBUNIT: Homotetramer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE
PHOSPHORIBOSYLTRANSFERASE FAMILY.
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CC
CC EMBL; M63983; AAA41350.1; -.
CC EMBL; S79292; AAB21288.1; -.
CC EMBL; X62085; CAA43997.1; -.
CC EMBL; AF001282; AAB65640.1; -.
CC EMBL; AF001278; AAB65640.1; JOINED.
CC EMBL; AF009655; AAB65640.1; JOINED.
CC EMBL; AF009656; AAB65640.1; JOINED.
CC EMBL; AF001279; AAB65640.1; JOINED.
CC EMBL; AF001280; AAB65640.1; JOINED.
CC EMBL; AF001281; AAB65640.1; JOINED.
CC FIR; S18140; S18140.
CC HSSP; P00492; 1HMP.

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DR	EMBL; AJ132697; CAB46657.1; -.
DR	HSP; P00492; IHMP.
DR	InterPro; IPR005904; Hxn_phspo trans.
DR	InterPro; IPR002375; Pr/PV_ip transf.
DR	InterPro; IPR000836; PRTransferase.
DR	Pfam; PF00156; Priboyltran; 1.
DR	TIGRFAMS; TIGR01203; HGPRTase; 1.
DR	PROSITE; PS00103; PUR_Pyr_PR_Transfer; 1.
KW	Transferase; Glycosyltransferase; Purine salvage; Magnesium.
FT	METAL 134 134 MAGNESIUM (BY SIMILARITY).
FT	METAL 135 135 MAGNESIUM (BY SIMILARITY).
SQ	SEQUENCE 218 AA; 24608 MW; 2229884B06AF727 CRC64;
Query Match	
Best Local Similarity 67.5%; Score 753; DB 1; Length 218;	
Matches 142; Conservative 32; Mismatches 38; Indels 0; Gaps	
QY	1 MATRSPGVIMDMPGVLDNLFYPOHYGDLVVLPHGIIIVDRTERLAKDIMKDIGY
DB	1 MATHSPCIVIGDDEQGYDLDLFCIPHYADDELEKVIIPHLIWDTERLAREIMKMGVGH
QY	61 DIMVLVLKGGYKFCADLVEHLKNISNRSDRFVSMKVDFIRLKYRNDQSMQEMQIIIGG
DB	61 HIVALCVLKGYYFFADLLDYIKALNRNSDKSPMTVDFIRLKYCNDQSTGDIKVIIGG
QY	121 DLSTLAKNFLIIVDVGGRTKALLSNIEKYKPNMKVASILLVXRTSRSDGFRPDYAC
DB	121 DLSTLTGKNVLIIVEDIIDTGKTKWTKLLSLKQYNPKMKVVASLLVXRTPSVGYRDFDFV
QY	181 FEIPHLFVVGVALDYNEFRDLNHHICVINEHG 212
DB	181 FEVPDRFVVGVALDYNEFRDLNHHICVISETG 212
RESULT 8	
HPRT SCHMA	
ID	HPRT SCHMA STANDARD; PRT; 284 AA.
AC	P09383;
DT	01-MAR-1989 (Rel. 10, Created)
DT	01-MAR-1989 (Rel. 10, Last sequence update)
DT	28-FEB-2003 (Rel. 41, Last annotation update)
DE	Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8) (HGPRPT
DE	(HGPRTase).
OS	HGPRT.
OS	Schistosoma mansoni (Blood fluke).
OC	Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeida
OC	Schistosomatidae; Schistosomatidae; Schistosoma.
OC	NCBI_TaxID=6183;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=Puerto Rican;
RX	MEDLINE=88303331; PubMed=3136439;
RA	Craig S.P., McKeerrow J.H., Newport G.N., Wang C.C.;
RT	"Analysis of cDNA encoding the hypoxanthine-guanine
RT	phosphoribosyltransferase (HGPRase) of Schistosoma mansoni; a
RT	putative target for chemotherapy.";
RT	Nucleic Acids Res. 16:7087-7101(1988).
RP	[2]
RP	SEQUENCE FROM N.A.
RC	STRAIN=Puerto Rican;
RX	MEDLINE=89160320; PubMed=2701934;
RA	Craig S.P., Muralidhar M.G., McKeerrow J.H., Wang C.C.;
RT	"Evidence for a class of very small introns in the gene for
RT	hypoxanthine-guanine phosphoribosyltransferase in Schistosoma
RT	mansoni.";
RT	Nucleic Acids Res. 17:1635-1647(1989).
CC	-!- CATALYTIC ACTIVITY: IMP + diphosphate = hypoxanthine + 5-phospho-
CC	alpha-D-ribose 1-diphosphate.
CC	-!- CATALYTIC ACTIVITY: GMP + diphosphate = guanine + 5-phospho-
CC	alpha-D-ribose 1-diphosphate.
CC	-!- PATHWAY: Purine salvage.
CC	-!- SUBUNIT: Homotetramer (By similarity).
CC	-!- SUBCELLULAR LOCATION: Cytoplasm (By similarity).





RA Heroux A., White E.L., Ross L.J., Borhani D.W.;

RT "Crystal structures of the Toxoplasma gondii hypoxanthine-guanine phosphoribosyltransferase-GMP and -IMP complexes: comparison of purine binding interactions with the XMP complex.";

RL Biochemistry 38:14485-14494(1999).

RN [4]

RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).

RX MEDLINE=20014542; PubMed=10545171;

RA Heroux A., White E.L., Ross L.J., Davis R.L., Borhani D.W.;

RT "Crystal structure of Toxoplasma gondii hypoxanthine-guanine phosphoribosyltransferase with bound XMP, pyrophosphate and two Mg<sup>2+</sup> ions: insights into the catalytic mechanism.";

RL Biochemistry 38:14495-14506(1999).

CC !- FUNCTION: CATALYZES THE MAGNESIUM ION DEPENDENT TRANSFER OF A RIBOSYL PHOSPHATE GROUP FROM PRPP TO THE N9 NITROGEN OF HYPOXANTHINE, GUANINE OR XANTHINE.

CC !- CATALYTIC ACTIVITY: IMP + diphosphate = hypoxanthine + 5-phospho-alpha-D-ribose 1-diphosphate.

CC !- CATALYTIC ACTIVITY: GMP + diphosphate = guanine + 5-phospho-alpha-D-ribose 1-diphosphate.

CC !- CATALYTIC ACTIVITY: 5-phospho-alpha-D-ribose 1-diphosphate + xanthine = (9-D-ribofuran-5'-phosphate + phosphate.

CC !- PATHWAY: Purine salvage.

CC !- SUBUNIT: HOMODIMER AT LOW IONIC STRENGTH AND HOMOTETRAMER AT HIGH IONIC STRENGTH.

CC !- SUBCELLULAR LOCATION: Cytoplasmic.

CC !- SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE PHOSPHORIBOSYLTRANSFERASE FAMILY.

CC -----

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DR EMBL; U09219; AA457068.1; --

DR PDB; 1DBR; 03-DEC-97.

DR PDB; 1QK3; 17-OCT-99.

DR PDB; 1QK4; 17-OCT-99.

DR PDB; 1QK5; 17-OCT-99.

DR PDB; 1FSG; 09-OCT-02.

DR InterPro; IPR005904; Hxn phpho trans.

DR InterPro; IPR002375; Pr/Pyr\_rp\_transf.

DR InterPro; IPR000836; PRTtransferase.

DR Pfam; PF00156; Pribosyltran; 1.

DR TIGRFAMs; TIGR01203; HGPRTase; 1.

DR PROSITE; PS00103; PUR PYR PR TRANSFER; 1.

KW Transferase; Glycosyltransferase; Purine salvage; Magnesium; 3D-structure.

KW 3D-structure.

FT METAL 146 146 MAGNESIUM.

FT METAL 147 147 MAGNESIUM.

FT HELIX 6 8

FT TURN 9 10

FT STRAND 11 11

FT TURN 12 14

FT STRAND 19 20

FT TURN 23 24

FT STRAND 27 28

FT HELIX 29 31

FT HELIX 36 41

FT STRAND 44 45

FT STRAND 47 47

FT HELIX 49 66

FT TURN 67 69

FT STRAND 72 77

FT TURN 81 82

FT HELIX 84 97

FT TURN 98 98

FT HELIX 100 102

FT TURN 103 104

FT STRAND 109 113

FT TURN 122 123

FT STRAND 130 130

FT HELIX 135 137

FT TURN 138 139

FT STRAND 141 149

FT HELIX 153 163

FT TURN 164 165

FT STRAND 169 178

FT TURN 183 184

FT STRAND 187 187

FT STRAND 190 195

FT STRAND 200 202

FT TURN 203 204

FT STRAND 205 205

FT TURN 208 213

FT STRAND 217 219

FT HELIX 222 226

FT TURN 227 227

SQ SEQUENCE 230 AA; 26386 MW; C3784254EF96361D CRC64;

Query Match 31.0%; Score 346; DB 1; Length 230;

Best Local Similarity 35.5%; Pred. No. 6.2e-22;

Matches 70; Conservative 49; Mismatches 74; Indels 4; Gaps 2;

QY 17 YDLNLTFTPOHYGLEYVLPHGIIVDRIERLAKDIMKDIGYSDIMVLVLKGGYKPCA 76

DB 27 YNADDFLVPCHCKPYDKILLPGLVKRVEKLAYDIHRTYFGEELHIICILKSGRFFN 86

QY 77 DVEVHLKNISSRDSFVSMKVDF---IRLKSRYNDOSMGEMQIIIGGDLSTLAGKNFLIV 133

DB 87 LLIDVLTATQKSGRESSVPPFEHYVRLKSVQNDNSTQQLTVL-SDDLISIFDKHVLIV 145

QY 134 EDVGTGRTMKALLNIEKYKPNMKVASLLVKRTSRSDGPRPDYAGFPIPHLFVVGYAL 193

DB 146 EDIVDTGFTLTFEGERLKAAGPKSMRIATLVKRTDRSNLSKGDVFVGFSIEDVWVGCCY 205

QY 194 DYNVEYFRDLNHCIVINE 210

DB 206 DFNEMFRDFDHVAVLSD 222

RESULT 12

HPRT\_BACSU STANDARD; PRT; 180 AA.

ID HPRT\_BACSU

AC P37472;

DT 01-OCT-1994 (Rel. 30, Created)

DT 01-OCT-1994 (Rel. 30, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8) (HGPRT)

DE (HGPRase).

GN HPRT OR HPT.

OS Bacillus subtilis.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI\_TaxID=1423;

RN [1]\_TaxID=1423;

RP SEQUENCE FROM N.A.

RC STRAIN=168;

RX MEDLINE=96051385; PubMed=7584024;

RA Ogasawara N., Nakai S., Yoshikawa H.;

RT "Systematic sequencing of the 180 kilobase region of the Bacillus subtilis chromosome containing the replication origin.";

RL DNA Res. 1:11-14(1994).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=168;

RX MEDLINE=98044033; PubMed=9384377;

RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T., Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,





[illegible]

```

RESULT 15
HGXR_TRIFO
ID ID HGXR_TRIFO STANDARD; PRT; 183 AA.
AC P51900;
DT DT 01-OCT-1996 (Rel. 34, Created)
DT DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DE Hypoxanthine-guanine-xanthine phosphoribosyltransferase (EC 2.4.2.-)
DE DE (HGXPRT) (HGXPRTase) (HGPRT).
GN GN HPT.
OS OS Trichichomonas foetus (Trichomonas foetus).
OC OC Eukaryota; Parabasalida; Trichomonadida; Trichomonadidae;
OC OC Trichichomonadinae; Trichichomonas.
OX OX NCBI_TaxID=5724;
[1]
RN RN SEQUENCE FROM N.A.
RC RC STRAIN=KV1;
RX RX MEDLINE=94277146; PubMed=8008020;
RA RA Chin M.S., Wang C.C.;
RT RT "Isolation, sequencing and expression of the gene encoding
RT RT hypoxanthine-guanine-xanthine phosphoribosyltransferase of
RT RT Trichichomonas foetus.";
RL RL Mol. Biochem. Parasitol. 63:221-229 (1994).
[2]
RN RN X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RP RP MEDLINE=96240318; PubMed=8679528;
RX RX Somoza J.R., Chin M.S., Focia P.J., Wang C.C., Fletterick R.J.;
EA EA "Crystal structure of the hypoxanthine-guanine-xanthine
RT RT phosphoribosyltransferase from the protozoan parasite Trichichomonas
RT RT foetus.";
RL RL Biochemistry 35:7032-7040(1996).

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DR EMBL; L08622; AAC37202.1; -.  
DR PDB; LHGX; 17-AUG-96.  
DR InterPro; IPR005904; Hxn\_phospho\_trans.  
DR InterPro; IPR002375; Pr/py\_rp\_transf.  
DR InterPro; IPR000836; Pmttransferase.  
DR Pfam; PF00156; Pribosyltran; 1.  
DR TIGRFAMs; TIGR01203; HGPrtase; 1.  
DR PROSITE; PS00103; PUR\_PYR\_PR\_TRANSFER; 1.  
KW Transferase; Glycosyltransferase; Purine salvage; Magnesium;  
KW 3D-structure.

FT METAL 102 102 MAGNESIUM.  
FT METAL 103 103 MAGNESIUM.  
FT TURN 8 9

FT STRAND 10 15

FT HELIX 17 35

FT TURN 36 38

FT STRAND 41 45

FT TURN 46 49

FT HELIX 50 57

FT TURN 58 59

FT STRAND 65 72

FT STRAND 87 87

FT TURN 94 95

FT STRAND 97 105

FT HELIX 109 119

FT TURN 120 121

FT STRAND 125 134

FT STRAND 147 152

FT TURN 157 159

FT STRAND 160 161

FT STRAND 162 162

FT STRAND 164 164

FT TURN 165 166

FT STRAND 167 167

FT TURN 169 170

FT STRAND 174 177

FT HELIX 179 183

SQ SEQUENCE 183 AA; A151E2FSD7D1C214 CRC64;

Query Match 21.0%; Score 234.5; DB 1; Length 183;  
Best Local Similarity 32.4%; Pred.No. 9.se-13;  
Matches 59; Conservative 37; Mismatches 73; Indels 13; Gaps 4;

QY 31 DLEYVLIPHGIIVDRIERLAKDKIMDKIGYSDIMVLCVLKGYKFCADLVEHLKNISRNSD 90

Db 9 DLERVLYNQDDIQKRIRELAELTEFYEYEDKNPNVICVLTGAVFFYTDLKHLD----- 61

QY 91 RFVSMKVDIFRLKSYRNDOSMGEMQIIGGGDLST-LAGKNFLIVEDVVGVTGRTMKALLSN 149

Db 62 --FQLEPDVVICSSYSGTKSTGNLTI--SKDLKTNIEGRHVLAVVEDIIDTGLTMYQLNN 117

QY 150 IEKYKPNMKVASLLVKRTSRDGRFP-DYAGFEIPLHFWGVYALDYNFYFDLNLHICVI 208

Db 118 LQMRKPEASLKVCTLCDKDGKXAYDVPIDYCGFVVENRYIIGYGFDFHKNYRNLPVIGIL 177

QY 209 NE 210

Db 178 KE 179

Search completed: November 13, 2003, 15:05:31  
Job time : 18 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 13, 2003, 15:02:56 ; Search time 35 Seconds  
(without alignments)  
1563.061 Million cell updates/sec

Title: US-09-902-705-2

Perfect score: 1116

Sequence: 1 MATRSPGVIMDDPFGVDLN.....LDYNEYFRDLNHCIVINEHG 212

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: sp\_archea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mbc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriaph:\*  
17: sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1065	95.4	225	4 Q9NRG1	Q9nrg1 homo sapien
2	786	70.4	218	11 Q60466	Q60466 cricetulus
3	782	70.1	218	11 Q99KF5	Q99kf5 mus musculus
4	779	69.8	218	11 Q64401	Q64401 cricetulus
5	746	66.8	210	11 Q9JK76	Q9jk76 akodon curs
6	658	59.0	186	6 Q9GJT9	Q9gjt9 bos taurus
7	553	49.6	161	11 Q9UK75	Q9uk75 akodon curs
8	543	48.7	154	6 Q46381	Q46381 oryctolagus
9	470	42.1	142	6 Q9XSI4	Q9xsi4 sus scrofa
10	456	40.9	135	6 Q28968	Q28968 sus scrofa
11	455	40.8	193	6 Q28530	Q28530 macropus ro
12	445.5	40.0	231	5 Q86085	Q86085 plasmodium
13	445.5	39.9	231	5 Q81J51	Q81j51 plasmodium
14	437	39.2	136	6 Q95258	Q95258 sus scrofa
15	430.5	38.6	214	5 Q9NF11	Q9nfl1 caenorhabdi
16	400	35.8	194	5 Q03925	Q03925 plasmodium

17	346	31.0	279	5	Q27375	Q27375 toxoplasma
18	306	27.4	84	6	Q29494	Q29494 macropus to
19	294	26.3	85	6	P79306	P79306 sus scrofa
20	290.5	26.0	115	11	O55061	O55061 mesocricetu
21	272	24.4	76	6	O97876	O97876 ornithorhyn
22	270.5	24.2	183	16	Q8XHL2	Q8xhl2 clostridium
23	265.5	23.8	180	16	Q9CFP9	Q9cff9 lactococcus
24	265	23.7	76	6	O97875	O97875 monodelphis
25	265	23.7	76	6	O97873	O97873 macropus eu
26	265	23.7	76	6	O97872	O97872 isodon mac
27	257.5	23.1	178	16	O97E91	O97eb1 clostridium
28	257.5	23.1	180	16	Q8P321	Q8p321 streptococc
29	257	23.0	176	16	Q8KC37	Q8kc97 chlorobium
30	254.5	22.8	648	16	Q32F56	Q32f56 listeria in
31	252	22.6	76	6	O97871	O97871 isodon mac
32	251.5	22.5	181	16	Q8R7L0	Q8r7l0 thermoaer
33	251.5	22.5	194	16	Q8NM82	Q8nm82 corynebacte
34	250.5	22.4	648	2	Q8KU03	Q8ku03 listeria mo
35	250.5	22.4	648	16	Q8YAC7	Q8yac7 listeria mo
36	247.5	22.2	180	16	Q97TC4	Q97tc4 streptococc
37	247.5	22.2	180	16	Q8DRP8	Q8drp8 streptococc
38	246.5	22.1	184	16	Q8EUI7	Q8eul7 oceanobacil
39	246	22.0	175	16	Q8RGK5	Q8rgk5 fusobacteri
40	245	22.0	76	6	O97874	O97874 macropus eu
41	244.5	21.9	175	2	Q9ZNK6	Q9znk6 clostridium
42	242.5	21.7	238	5	Q95ZC9	Q95zc9 leishmania
43	241	21.6	212	16	Q8FMG1	Q8fmgl corynebacte
44	239.5	21.5	179	16	Q99W93	Q99w93 staphylococ
45	239	21.4	241	5	Q9U6Y2	Q9u6y2 leishmania

#### ALIGNMENTS

#### RESULT 1

Q9NRG1 PRELIMINARY; PRT; 225 AA.  
AC Q9NRG1  
DT 01-OCT-2000 (TREMELrel. 15, Created)  
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)  
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)  
DE HHGP (HHGP protein).  
GN HHGP.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver cancer;  
RA Li Y., Wu T., Xu S., Ren S., Chen Z., Han Z.;  
RT "A novel gene expressed in human liver cancer tissue."  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,  
RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,  
RA Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,  
RA Arita M., Nabeekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,  
RA Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;  
RT "NED0 human cDNA sequencing project."  
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Eye;  
RA Strausberg R.;  
RT Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF226056; AAF6956.1; -;  
DR EMBL; AK021950; BAB13944.1; -;  
DR EMBL; BC008662; AAH08662.1; -;  
DR HSSP; P00492; 1HMP.  
DR InterPro; IPR005904; Hxn\_phospho\_trans.

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DR InterPro; IPR000836; PRtransferase.
DR Pfam; PF00156; Pribosyltran; 1.
DR TIGRFAMs; TIGR01203; HGPRTase; 1.
KW Transferase
SQ SEQUENCE 225 AA; 25673 MW; CD612C2783AC3071 CRC64;
Query Match 95.4%; Score 1065; DB 4; Length 225;
Best Local Similarity 98.5%; Pred. No. 1.2e-86;
Matches 203; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 7 GVIMDWPQGYDLNLFYTPQHYGDLVLPQHYGVLEVLPHGIIVDRIERLAKDINKDIIGYSDIWLIC 66
DB 14 GVIMDWPQGYDLNLFYTPQHYGDLVLPQHYGVLEVLPHGIIVDRIERLAKDINKDIIGYSDIWLIC 73
QY 67 VLKGGYKFCADLVEHLKNIISNSDRFVSMKVDYFIRLKSRYNDQSGEMQIIGGGDLSTIA 126
DB 74 VLKGGYKFCADLVEHLKNIISNSDRFVSMKVDYFIRLKSRYNDQSGEMQIIGGGDLSTIA 133
QY 127 GKFNFLIVEDVVGTRGTMTKALLSNIEKYKPNMKVASLLVVKRTSRSDGFRPDYAGFEIPLH 186
DB 134 GKFNFLIVEDVVGTRGTMTKALLSNIEKYKPNMKVASLLVVKRTSRSDGFRPDYAGFEIPLN 193
QY 187 FVVGALDYNEFYFRDLNHCIVINEHG 212
DB 194 FVVGALDYNEFYFRDLNHCIVINEHG 219
RESULT 2
Q60466
ID Q60466 PRELIMINARY; PRT; 218 AA.
AC Q60466;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypoxanthine (Guanine) phosphoribosyltransferase.
GN HPT.
OS Cricetus longicaudatus (Long-tailed hamster) (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_TaxID=10030;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=V79;
RX MEDLINE=93313862; PubMed=8324741;
RA Wei S.J.C., Chang R.L., Bhachech N., Cui X.X., Merkler K.A.,
RA Wong C.O., Hennig E., Yagi H., Jerina D.M., Conney A.H.;
RT "Dose-dependent differences in the profile of mutations induced by
RT (+)-7R,8S-Dihydroxy-9S,10R-epoxy-7,8,9,10-tetrahydrobenzo-(a) pyrene
RT in the coding region of the Hypoxanthine (Guanine)
RT Phosphoribosyltransferase gene in chinese hamster V-79 cells.";
RL Cancer Res. 53:3294-3301(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=V79;
RA Wei S.C.;
RL Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE
CC PHOSPHORIBOSYLTRANSFERASE FAMILY.
DR EMBL; X59652; CAA42198.1; -.
DR HSSP; P00492; 1BZY
DR InterPro; IPR005904; Hxn_phospho_trans.
DR InterPro; IPR002375; Pr/py_rp_transf.
DR InterPro; IPR000836; PRtransferase.
DR Pfam; PF00156; Pribosyltran; 1.
DR TIGRFAMs; TIGR01203; HGPRTase; 1.
DR PROSITE; PS00103; PUR_PVR_PR_TRANSFER; 1.
KW Glycosyltransferase,Transferase.
SQ SEQUENCE 218 AA; 24627 MW; 319A7A76992B750D CRC64;
Query Match 70.4%; Score 786; DB 11; Length 218;
Best Local Similarity 69.3%; Pred. No. 6.8e-62;
Matches 147; Conservative 30; Mismatches 35; Indels 0; Gaps 0;
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QY 1 MATRSPGVIMDDWPQGYDLNLFYTPQHYGDLVLPQHYGVLEVLPHGIIVDRIERLAKDINKDIIGY 60
DB 1 MATRSPSVVISDDEPGYDLDLFCIPNHYVEDEKVFIPHGVIIMDTERLARDVNMKGH 60
QY 61 DIMVLVLKGGYKFCADLVEHLKNIISNSDRFVSMKVDYFIRLKSRYNDQSGEMQIIGGG 120
DB 61 HIVALCVLKGGYKFCADLVEHLKNIISNSDRSIPMTVDYFIRLKSRYNDQSGTDIKVIGGD 120
QY 121 DLSTLAGKNFLIVEDVVGTRGTMTKALLSNIEKYKPNMKVASLLVVKRTSRSDGFRPDYAG 180
DB 121 DLSTLTGKNVLIVEDIIDTGKTMQTLTLVKRYNPKMKVASLLVVKRTSRSGVGRPDFVG 180
QY 181 FEIPLHFVVGALDYNEFYFRDLNHCIVINEHG 212
DB 181 FEIPDKFVVGALDYNEFYFRDLNHCIVISGTG 212
RESULT 3
Q99KF5
ID Q99KF5 PRELIMINARY; PRT; 218 AA.
AC Q99KF5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypoxanthine guanine phosphoribosyl transferase.
GN HPT.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE
CC PHOSPHORIBOSYLTRANSFERASE FAMILY.
DR EMBL; BC004686; AAH04686.1; -.
DR HSSP; P00492; 1HMP.
DR MGD; MGI:96217; Hprt.
DR InterPro; IPR005904; Hxn_phospho_trans.
DR InterPro; IPR002375; Pr/py_rp_transf.
DR InterPro; IPR000836; PRtransferase.
DR Pfam; PF00156; Pribosyltran; 1.
DR TIGRFAMs; TIGR01203; HGPRTase; 1.
DR PROSITE; PS00103; PUR_PVR_PR_TRANSFER; 1.
KW Glycosyltransferase,Transferase.
SQ SEQUENCE 218 AA; 24544 MW; 83F6DA7507787FA4 CRC64;
Query Match 70.1%; Score 782; DB 11; Length 218;
Best Local Similarity 68.9%; Pred. No. 1.5e-61;
Matches 146; Conservative 31; Mismatches 35; Indels 0; Gaps 0;
QY 1 MATRSPGVIMDDWPQGYDLNLFYTPQHYGDLVLPQHYGVLEVLPHGIIVDRIERLAKDINKDIIGY 60
DB 1 MATRSPSVVISDDEPGYDLDLFCIPNHYAEDEKVFIPHGVIIMDTERLARDVNMKGH 60
QY 61 DIMVLVLKGGYKFCADLVEHLKNIISNSDRFVSMKVDYFIRLKSRYNDQSGEMQIIGGG 120
DB 61 HIVALCVLKGGYKFCADLVEHLKNIISNSDRSIPMTVDYFIRLKSRYNDQSGTDIKVIGGD 120
QY 121 DLSTLAGKNFLIVEDVVGTRGTMTKALLSNIEKYKPNMKVASLLVVKRTSRSDGFRPDYAG 180
DB 121 DLSTLTGKNVLIVEDIIDTGKTMQTLTLVKRYNPKMKVASLLVVKRTSRSGVGRPDFVG 180
QY 181 FEIPLHFVVGALDYNEFYFRDLNHCIVINEHG 212
DB 181 FEIPDKFVVGALDYNEFYFRDLNHCIVISGTG 212
RESULT 4
Q64401
ID Q64401 PRELIMINARY; PRT; 218 AA.
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AC Q64401;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypoxanthine guanine phosphoribosyltransferase (EC 2.4.2.8).
GN HPT.
OS Cricetus longicaudatus (Long-tailed hamster) (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_TaxID=10030;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Rossiter F., Muzny M., Caskey T., Fox M.;
RT "A Chinese hamster HPRT point mutation reverts to the wild-type
RT sequence.";
RL Submitted (NOV-1989) to the EMBL/GenBank/DBJ databases.
DR EMBL; X17656; CAA35648.1; -.
DR HSSP; P00492; IHMP.
DR InterPro; IPR005904; Hxn_phospho_trans.
DR TIGRFAMs; TIGR01203; HGPRTase; 1.
DR TIGRFAMs; TIGR01203; HGPRTase; 1.
KW Glycosyltransferase; Transferase.
SQ SEQUENCE 218 AA; 24569 MW; A2A97A74P6D6E762 CRC64;

Query Match 69.8%; Score 779; DB 11; Length 218;
Best Local Similarity 68.9%; Pred. No. 2.8e-61;
Matches 146; Conservative 30; Mismatches 36; Indels 0; Gaps 0;

Qy 1 MATSPGVIMDDWPGYDLNLFYPOHYGDLVLEVLPHGIIIVDRIERLAKDIMKDIYS 60
Db 1 MATSPGVISDDDFGYDLDFCIPNHYVELEKVFIEPHGLMDRTERLARDVNMKGH 60

Qy 61 DIMVLVCKGGYKFCADLVEHLKNISRNSDRFVSMKVDFIRLKSRYNDQSMGEQIIGG 120
Db 61 HIVALVLKGGYKFCADLVDLYIKALNRNSDRIPMTVDFIRLKSRYNDQSGDKIVIGD 120

Qy 121 DLSTLAGNFLIVDVGTGTMTKALLSNIKYPKNMKVASLLVKRTSRSDGFRPDYAG 180
Db 121 DLSTLTGNVLIVEGIIDTGTMTQTLISLVKQYNPKVKVASLLVKRTSRSGVGRPDVG 180

Qy 181 FEIPLHFLVGVGALDYNEFRDLNHCIVNEHG 212
Db 181 FEIPDKFVGVGALDYNEFRDLNHCIVISETG 212

RESULT 5
Q9JK76 PRELIMINARY; PRT; 210 AA.
AC Q9JK76;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypoxanthine phosphoribosyltransferase (Fragment).
GN HPT.
OS Akodon cursor.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Akodon.
OX NCBI_TaxID=29096;
RN [1]
RP SEQUENCE FROM N.A.
RA Bonvicino C.R.B., Moreira M.A.M., Arcuri R.A., Seunaez H.N.;
RT "Induction and Characterization of Hypoxanthine
RT Phosphoribosyltransferase (hprt) Deficient Cell Lines of Akodon
RT cursor.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE
CC PHOSPHORIBOSYLTRANSFERASE FAMILY.
DR EMBL; AF254383; AAF70286.1; -.
DR HSSP; P00492; 1B2Y.
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DR InterPro; IPR005904; Hxn_phospho_trans.
DR InterPro; IPR002375; Pr/PY_rp_transf.
DR Pfam; PF00156; PriBosyltran; 1.
DR TIGRFAMs; TIGR01203; HGPRTase; 1.
DR PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.
KW Glycosyltransferase; Transferase.
FT NON_TER 1
SQ SEQUENCE 210 AA; 23827 MW; CPE3D9270E8048AB CRC64;

Query Match 66.8%; Score 746; DB 11; Length 210;
Best Local Similarity 68.1%; Pred. No. 2.3e-58;
Matches 139; Conservative 30; Mismatches 35; Indels 0; Gaps 0;

Qy 9 VIMDDWPGYDLNLFYPOHYGDLVLEVLPHGIIIVDRIERLAKDIMKDIYS 68
Db 1 VISDDPGYDLDFCIPNHYIEDLEKVFIEPHGLMDRTERLARDVNMKGHIIVALCVL 60

Qy 69 KGGYKFCADLVEHLKNISRNSDRFVSMKVDFIRLKSRYNDQSMGEQIIGGDLSTLACK 128
Db 61 KGGYKFFTDLLDYTKALNRNSDRIPMTVDFIRLKSRYNDQSGDKIVIGDGLSTLTGK 120

Qy 129 NFLIVEDVVGTRTMTKALLSNIKYPKNMKVASLLVKRTSRSDGFRPDYAGFEIPLHFLV 188
Db 121 NVLIVEDIIDTGTMTQTLISLVKQYNPKVKVASLLVKRTSRSGVGRPDVGFPEIPDKFV 180

Qy 189 VGYALDYNEFRDLNHCIVNEHG 212
Db 181 VGYALDYNEFRDLNHCIVISETG 204

RESULT 6
Q9GJT9 PRELIMINARY; PRT; 186 AA.
AC Q9GJT9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypoxanthine phosphoribosyltransferase (Fragment).
GN HPRT.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE OF 1-23 FROM N.A.
RC TISSUE=Liver;
RA Poloumienko A., Blecher S.R.;
RT "Exon-intron structure of mammalian HPRT genes.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Poloumienko A., Blecher S.;
RT "Intron-exon structure of bovine and swine HPRT genes.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE
CC PHOSPHORIBOSYLTRANSFERASE FAMILY.
DR EMBL; AF294360; AAG18424.1; -.
DR EMBL; AF294354; AAG18424.1; JOINED.
DR EMBL; AF294355; AAG18424.1; JOINED.
DR EMBL; AF294356; AAG18424.1; JOINED.
DR EMBL; AF294357; AAG18424.1; JOINED.
DR EMBL; AF294358; AAG18424.1; JOINED.
DR EMBL; AF294359; AAG18424.1; JOINED.
DR EMBL; AF176419; AAG09236.1; -.
DR HSSP; P00492; IHMP.
DR InterPro; IPR005904; Hxn_phospho_trans.
DR InterPro; IPR002375; Pr/PY_rp_transf.
DR TIGRFAMs; TIGR01203; HGPRTase; 1.
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DR PROSITE; PS00103; PUR\_PYR\_PR\_TRANSFER; 1.  
KW Glycosyltransferase; Transferase.  
FT NON\_TER 186 186  
FT NON\_TER 186 186  
SQ SEQUENCE 186 AA; 20993 MW; 546486338FC42865 CRC64;  
  
Query Match 59.0%; Score 658; DB 6; Length 186;  
Best Local Similarity 65.1%; Pred. No. 1.3e-50;  
Matches 121; Conservative 32; Mismatches 33; Indels 0; Gaps 0;  
  
Qy 15 PGYDLNLFYQHYXGDLVLYLPHGIIVDRIERLAKDIMKDIGYSDIMVLVCKGGYKF 74  
Db 1 PGYDLNLFYQHYXGDLVLYLPHGIIVDRIERLAKDIMKDIGYSDIMVLVCKGGYKF 60  
Qy 75 CADLVEHLKNISSRDSFVSMKVPFIRLKSRYNDQSGEMQIIGGGDLSTLAGKNFLIVE 134  
Db 61 FADLLDYIKALNRNSDRSIPMTVDIFIRLKSRYNDQSGEMQIIGGGDLSTLAGKNFLIVE 120  
Qy 135 DVVGTGRTMKALLSNIKYKNNMIKVASLLVKTSSRSGFRPDYAGFPIHLFVVGVALD 194  
Db 121 DIIDTGTMTQTLALVKKHPKVKVASLLMKTTPRSVGYKPDFVGFPIPKFVVGVALD 180  
Qy 195 YNEYFR 200  
Db 181 YNEYSR 186  
  
RESULT 7  
Q9JK75 PRELIMINARY; PRT; 161 AA.  
AC Q9JK75  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Mutant hypoxanthine phosphoribosyltransferase (Fragment).  
GN HPRT.  
OS Akodon cursor.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;  
OC Akodon.  
OX NCBI\_TaxID=29096;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Bonvicino C.R.B., Moreira M.A.M., Arcuri R.A., Seunaez H.N.;  
RT "Induction and Characterization of Hypoxanthine  
RT Phosphoribosyltransferase (hppt) Deficient Cell Lines of Akodon  
RT cursor."  
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE  
CC PHOSPHORIBOSYLTRANSFERASE FAMILY.  
DR EMBL; AF254384; AAF70287.1; -.  
DR HSSP; P00492; 1BZY.  
DR InterPro; IPR005904; Hxn\_phospho\_trans.  
DR InterPro; IPR002375; Pr/PY\_ip\_transf.  
DR InterPro; IPR000836; PRTtransferase.  
DR Pfam; PF00156; Pribo syltran; 1.  
DR TIGRFAMs; TIGR01203; HGPrtase; 1.  
DR PROSITE; PS00103; PUR\_PYR\_PR\_TRANSFER; 1.  
KW Glycosyltransferase; Transferase.  
FT NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 161 AA; 18153 MW; FE8305EAF248EF17 CRC64;  
  
Query Match 49.6%; Score 553; DB 11; Length 161;  
Best Local Similarity 64.6%; Pred. No. 2.3e-41;  
Matches 104; Conservative 27; Mismatches 30; Indels 0; Gaps 0;  
  
Qy 9 VIMDDWPGYDNLFTYPOHYXGDLVLYLPHGIIVDRIERLAKDIMKDIGYSDIMVLVCL 68  
Db 1 VISDEPGYDNLFTYPOHYXGDLVLYLPHGIIVDRIERLAKDIMKDIGYSDIMVLVCL 60  
Qy 69 KGGYKFCADLVEHLKNISSRDSFVSMKVPFIRLKSRYNDQSGEMQIIGGGDLSTLAGK 128  
Db 61 KGGYKFFTDLLDYIKALNRNSDRSIPMTVDIFIRLKSRYNDQSGEMQIIGGGDLSTLAGK 120

Qy 129 NFLIVEDVVGTRTKALLSNIKYKNNMIKVASLLVKTSS 169  
Db 121 NVLVEDIIDTGTMTQTLALVKKHPKVKVASLLVKTSS 161  
  
RESULT 8  
O46381 PRELIMINARY; PRT; 154 AA.  
ID O46381  
AC O46381  
DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Hypoxanthine phosphoribosyltransferase (Fragment).  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=New Zealand White;  
RA Boykiw R.H., Sciore P., Reno C., Marchuk L., Frank C.B., Hart D.A.;  
RT "Cloning, sequencing, and expression of extracellular matrix molecules  
RT in normal and healing rabbit ligament by RT-PCR."  
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE  
CC PHOSPHORIBOSYLTRANSFERASE FAMILY.  
DR EMBL; AF020294; AAB87864.1; -.  
DR HSSP; P00492; 1HMP.  
DR InterPro; IPR005904; Hxn\_phospho\_trans.  
DR InterPro; IPR002375; Pr/PY\_ip\_transf.  
DR InterPro; IPR000836; PRTtransferase.  
DR Pfam; PF00156; Pribo syltran; 1.  
DR TIGRFAMs; TIGR01203; HGPrtase; 1.  
DR PROSITE; PS00103; PUR\_PYR\_PR\_TRANSFER; 1.  
KW Glycosyltransferase; Transferase.  
FT NON\_TER 1  
FT NON\_TER 154  
SQ SEQUENCE 154 AA; 17326 MW; FDBD6F796DF07B2A CRC64;  
  
Query Match 48.7%; Score 543; DB 6; Length 154;  
Best Local Similarity 66.2%; Pred. No. 1.7e-40;  
Matches 102; Conservative 27; Mismatches 25; Indels 0; Gaps 0;  
  
Qy 42 IVDRIERLAKDIMKDIGYSDIMVLVCKGGYKFCADLVEHLKNISSRDSFVSMKVPFIR 101  
Db 1 IMDRTERLARDVMKEMGGHIVALCVLKGKYPFADLLDYIKALNRNSDRSIPMTVDIFIR 60  
Qy 102 LKSYRNDQSGEMQIIGGGDLSTLAGKNFLIVEDVVGTRTKALLSNIKYKNNMIKVA 161  
Db 61 LKSYCNDQSGTDGIKVIIGGGDLSTLAGKNFLIVEDVVGTRTKALLSNIKYKNNMIKVA 120  
Qy 162 SLLVKTSSRSGFRPDYAGFPIHLFVVGVALDY 195  
Db 121 SLLVKTTPRSVGYRPDFVGFPIPKFVVGVALDY 154  
  
RESULT 9  
O9XS14 PRELIMINARY; PRT; 142 AA.  
ID O9XS14  
AC O9XS14  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Hypoxanthine phosphoribosyltransferase (Fragment).  
OS Sus scrofa (pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Landrace x Large White;  
RA Gyoerify A., Steinborn R., Baiaasz M., Plana-Duran J., Klein D.,

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RA Mueller M., Brem G.;
RL "Variant pHPT sequence.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE
CC PHOSPHORIBOSYLTRANSFERASE FAMILY.
DR EMBL; AF143818; AAD30159.1; -.
DR HSSP; P00492; IHMP.
DR InterPro; IPR002375; Pr/PY_rp.transf.
DR InterPro; IPR000836; Prtransferase.
DR Pfam; PF00156; Pribosyltran; 1.
DR PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.
KW Glycosyltransferase; Transferase.
FT NON_TER 1
FT NON_TER 142
FT NON_TER 142
SQ SEQUENCE 142 AA; 15365 MW; 4FA8CBB7D25F4983 CRC64;

Query Match 42.1%; Score 470; DB 6; Length 142;
Best Local Similarity 61.3%; Pred. No. 4.5e-34;
Matches 87; Conservative 28; Mismatches 27; Indels 0; Gaps 0;

QY 20 NLTYPQHYGDLEVLPHGIIIVDRIBRLAKDINKDGYSDIMVLCVKGKGFADLV 79
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 DLFCIPHYAEDLEKVFIFPHGLIMDRTERLARDVMKMGHIVALCVLKGKGFADLL 60
QY 80 EHLKNJSRNSDRFVSMKVDFIRLKSRYNDQSGMGMQIIGGDLSTLACKNFIIVDVG 139
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 DYIKALNRNSDRSIPMTVDFIRLKSRYCNDQSTGDIKVIIGGDLSTLTKNVLIVEDI 120

QY 140 GRTMKALLSNIKEYKPNMKVA 161
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
121 GKTWQTLTSLVKQHNPKMKVA 142

RESULT 10
Q28968 PRELIMINARY; PRT; 135 AA.
AC Q28968;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypoxanthine phosphoribosyltransferase (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Foss D.L., Murtaugh M.P.;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Foss D.L., Murtaugh M.P.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE
CC PHOSPHORIBOSYLTRANSFERASE FAMILY.
DR EMBL; U32316; AAB03248.1; -.
DR HSSP; P00492; IHMP.
DR InterPro; IPR005904; Hxn_phospho.trans.
DR InterPro; IPR002375; Pr/PY_rp.transf.
DR InterPro; IPR000836; Prtransferase.
DR Pfam; PF00156; Pribosyltran; 1.
DR TIGRfams; TIGR01203; HGPRase; 1.
DR PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.
KW Glycosyltransferase; Transferase.
FT NON_TER 1
FT NON_TER 135
FT NON_TER 135
SQ SEQUENCE 135 AA; 15017 MW; E758F6B0B090F9A09 CRC64;

Query Match 40.9%; Score 456; DB 6; Length 135;
Best Local Similarity 63.0%; Pred. No. 7.5e-33;
Matches 85; Conservative 27; Mismatches 23; Indels 0; Gaps 0;

QY 47 ERLAKDTMKDGYSDIMVLCVKGKGFADLVHLKNISNRNSDRFVSMKVDFIRLKS 106
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 ERLARDVMKMGHIVALCVLKGKGFADLLDYIKALNRNSDTSIPMTVDFIRLKS 60
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QY 107 NDQSGMGMQIIGGDLSTLACKNFIIVDVGRTGRTMKALLSNIKEYKPNMKVASLLVK 166
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 NDQSTGDIKVIIGGDLSTLTKGNVLIVEDIIDTGTQTLTSLVKQHNPKMKVASLLVK 120

QY 167 RTSRSDGFRPDYAGF 181
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:
121 RTPRSVGYRPFVGF 135

RESULT 11
Q28530 PRELIMINARY; PRT; 193 AA.
AC Q28530; Q29493;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypoxanthine phosphoribosyltransferase (EC 2.4.2.8) (Hypoxanthine-
guanine phosphoribosyltransferase) (HGPTrase) (IMP pyrophosphorylase)
DE (TRANSPHOSPHORIBOSIDASE) (Guanine phosphoribosyltransferase)
DE (Fragment).
OS Macropus robustus (Wallaroo) (Euro).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=9319;
RN [1]
RP SEQUENCE FROM N.A.
RA Conaty J., Piper A.;
OC TISSUE=Liver;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 166-187 FROM N.A.
RX MEDLINE=93289446; PubMed=7685549;
RA Piper A.A., Bennett A.M., Noyce L., Swanton M.K., Cooper D.W.;
RT "Isolation of a clone partially encoding hill kangaroo X-linked
hypoxanthine phosphoribosyltransferase: sex differences in methylation
in the body of the gene.";
RT Somat. Cell Mol. Genet. 19:141-159(1993).
CC -!- CATALYTIC ACTIVITY: IMP + DIPHOSPHATE = HYPOXANTHINE + 5-PHOSPHO-
ALPHA-D-RIBOSE 1-DIPHOSPHATE.
DR EMBL; L41993; AAA81355.1; -.
DR EMBL; M77683; AAA31600.1; -.
DR HSSP; P00492; IHMP.
DR InterPro; IPR000836; Prtransferase.
DR Pfam; PF00156; Pribosyltran; 1.
KW Glycosyltransferase; Transferase.
FT NON_TER 1
FT NON_TER 193
FT NON_TER 193
SQ SEQUENCE 193 AA; 21153 MW; 2C1DA5037FASF010 CRC64;

Query Match 40.8%; Score 455; DB 6; Length 193;
Best Local Similarity 64.2%; Pred. No. 1.5e-32;
Matches 86; Conservative 22; Mismatches 26; Indels 0; Gaps 0;

QY 1 MATSPGVIMDDWPGVDLNLFTYPQHYGDLVLPVPHGIIIVDRIBRLAKDINKDGY 60
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
60 MANLSPSIVIEDDEPGYDLDFCIPKHYAQDLKVFIFPHGLIMDRTERLARDVMKMG 119

QY 61 DIMVLCVKGKGFADLVHLKNISNRNSDRFVSMKVDFIRLKSRYNDQSGMGMQIIGG 120
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
120 HIVALCVLKGKGFADLLDYIKALNRNSDKSIPMTVDFIRLKSRYCNDQSTGDIKVI 179

QY 121 DLSTLACKNFIIV 134
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:
180 DLSTLTKGNVLIV 193

RESULT 12
Q96085 PRELIMINARY; PRT; 231 AA.
AC Q96085;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
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DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypoxanthine-guanine phosphoribosyl transferase (HGPRt).
GN HGPRt.
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=XAT;
RX MEDLINE=21165804; PubMed=11269277;
RA Onda T., Miyamoto K., Sugioke Y., Kangawa K., Kano S., Suzuki M.;
RT "Suppressed expression of hypoxanthine-guanine
RT phosphoribosyltransferase (HGPRt) in an irradiation-attenuated
RT Plasmodium berghei XAT strain.";
RL Parasitol. Int. 48:157-167(1999).
CC -!- SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE
CC PHOSPHORIBOSYLTRANSFERASE FAMILY.
DR EMBL; AB020413; BAA34691.1; -.
DR HSSP; P20035; 1CJB.
DR InterPro; IPR005904; Hxn_phospho_trans.
DR InterPro; IPR002375; Pr/py_rp_transf.
DR InterPro; IPR000836; PRTtransferase.
DR Pfam; PF00156; Pribosyltran; 1.
DR TIGRfam; TIGR01203; HGPRtase; 1.
DR PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.
DR GlycoSyLtransferase; Transferase.
SQ SEQUENCE 231 AA; 26525 MW; C028F5E45CDB8B72 CRC64;

Query Match 40.0%; Score 446.5; DB 5; Length 231;
Best Local Similarity 42.7%; Pred. No. 1.1e-31;
Matches 91; Conservative 41; Mismatches 66; Indels 15; Gaps 4;

Qy 8 VVIMDDPGYDLNLTFTYPQHYGDLVYLPHGIIIVDRIERLAKDIMKDIYSDIMVLCV 67
Db 17 VMIKDD-DGVEFDSFTPDHYKNVLYKRLIPNGLIKSRVERMAFDISRTYNGEFLHLL 75
Qy 68 LKGGYKFCADLVEHLKNI-----SRNSDRFVSMKVDFIRLKSRYNDQSMGEMQIIGG 119
Db 76 LKGRSFRFTSLKLYDLRIHNYIADASTNSR-----BHYVRVKSVCNTQSTGLRLEV-S 129
Qy 120 GDLSTLAGKNFLIVDDVGTGRTMKALLSNIEKYKPNMKIVASLLVKRTSRSDGFRPDYA 179
Db 130 EDLSCLGKGNLIVEDIIDTGNLTSLKFCDYLLKKFEKPTIAVSALYIKHTPLWNGFKADFT 189
Qy 180 GFEIPEHLFVVGVALDYNEYPFDLNHICVINEHG 212
Db 190 GFSVPENFLVGCGLDYNEFRDLNHLVCIISSEG 222

RESULT 13
ID Q81J51 PRELIMINARY; PRT; 231 AA.
AC Q81J51
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Hypoxanthine phosphoribosyltransferase.
GN Pf10_0121.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RX MEDLINE=22255705; PubMed=12368864;
RA Gardner M.J., Hall N., Fung E., White O., Bowman S., Paulsen I.T., James K.,
RA Carlton J.M., Pain A., Nelson K.E., Salzberg S.L., Craig A., Kyes S.,
RA Eisen J.A., Rutherford K., Salzberg S.J., Suh B., Peterson J., Angiuoli S.,
RA Chan M.-S., Nene V., Shallog J., Haft D., Mather M.W., Vaidya A.B.,
RA Perte A., Allen J., Salengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
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RA Fraser C.M., Barrell B.;
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum.";
RL Nature 419:498-511(2002).
DR EMBL; AE014830; AAN35319.1; -.
DR Transferase; Glycosyltransferase..
SQ SEQUENCE 231 AA; 26362 MW; BC6D3B30486DD287 CRC64;

Query Match 39.9%; Score 445.5; DB 5; Length 231;
Best Local Similarity 42.7%; Pred. No. 1.3e-31;
Matches 93; Conservative 40; Mismatches 74; Indels 11; Gaps 3;

Qy 5 SPGV-----VIMDDPGYDLNLTFTYPQHYGDLVYLPHGIIIVDRIERLAKDIMKDI 57
Db 6 NPGAGENAFDPVFVKDDGDYDLSFMIPAHYKYLTKLVLPNGVGIKNRIEKLAYDIKKVY 65
Qy 58 GYSIDIMVLCVKGKFCADLVEHLKNI SRNSDRFVSMKV--DFIRLKSRYNDQSMGEM 114
Db 66 NNEEFHILCLLKGSRGFTALLKHLRIHNSAVETSKPLFGEHYVRVKSVCNDQSTGTL 125
Qy 115 QIIIGGDLSTLAGKNFLIVDDVGTGRTMKALLSNIEKYKPNMKIVASLLVKRTSRSDGF 174
Db 126 EIV-SEDLSCCLKGKHLVIEDIIDTKTLVKFCEVLLKKFEIKTVAIACLFIKRTPLWNGP 184
Qy 175 RPYAGFEIPEHLFVVGVALDYNEYPFDLNHICVINEHG 212
Db 185 KADFVGFSPDPHFVVGYSLDYNEIFRDLDHCCLVNDEG 222

RESULT 14
Q95258 PRELIMINARY; PRT; 136 AA.
ID Q95258
AC Q95258;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypoxanthine phosphoribosyltransferase (Fragment).
GN HPRT.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Mansfield L.;
RT "Porcine HPRT sequence.";
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE
CC PHOSPHORIBOSYLTRANSFERASE FAMILY.
DR EMBL; U69731; AAB16389.1; -.
DR HSSP; P00492; 1HMP.
DR InterPro; IPR002375; Pr/py_rp_transf.
DR InterPro; IPR000836; PRTtransferase.
DR Pfam; PF00156; Pribosyltran; 1.
DR PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.
DR GlycoSyLtransferase; Transferase.
FT NON_TER 1
FT NON_TER 136
SQ SEQUENCE 136 AA; 15399 MW; D531783C182A1FF7 CRC64;

Query Match 39.2%; Score 437; DB 6; Length 136;
Best Local Similarity 63.1%; Pred. No. 3.7e-31;
Matches 82; Conservative 26; Mismatches 22; Indels 0; Gaps 0;

Qy 47 ERLAKDIMKDIYSDIMVLCVKGKFCADLVEHLKNI SRNSDRFVSMKVDFIRLKSRY 106
Db 1 ERLAQRVWKEMGGHHIIVALCVLKGKFFADLLDIYKALNNSDRSPMTVDVDFRLKSYC 60
Qy 107 NDQSMGEMQIIGGDLSTLAGKNFLIVDDVGTGRTMKALLSNIEKYKPNMKIVASLLVK 166
Db 61 NDQSTGDIKVIIGGDLSTLAGKNFLIVEDIIDTKTQTLTLLSLVKQHPKMKVVASLLVK 120
Qy 167 RTSRSDGFRP 176
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 4, 2003, 12:13:13 ; Search time 2584 Seconds  
(without alignments)  
3356.363 Million cell updates/sec

Title: US-09-902-705-2  
Perfect score: 1116  
Sequence: 1 MATRSPGVIMDDPCYDLN.....LDYNEYPDLNHCIVINEHG 212

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Zgapop 6.0 , Zgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+\_p2n.model -DEV=xlp

Q=/cgn2\_1/USPTO\_spool\_p/US09902705/runat\_03102003\_085505\_27968/app\_query.fasta\_1  
391  
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-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DLEXT=7

Database : GenEmbl:\*  
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2: gb\_htg:\*  
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9: gb\_px:\*  
10: gb\_ro:\*

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12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*  
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32: em\_htg\_other:\*  
33: em\_htg\_mus:\*  
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40: em\_htgo\_mus:\*  
41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1065	95.4	807	9	AF226056
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4	1065	95.4	1926	6	BD159230
5	1065	95.4	1926	9	AK021950
6	1038	93.0	783	6	BD146172
7	786	70.4	657	10	CLHPRT
8	783	70.2	702	10	MUSHPRTS
9	782	70.1	1281	10	BC004686
10	779	69.8	685	9	S43335
11	779	69.8	1222	10	CLHPRTM
12	779	69.8	1316	9	BC000578
13	779	69.8	1331	9	HSHPRT
14	779	69.8	1331	9	HUMHPT
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AR310478 Sequence  
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BC008662 Homo sapi  
BD159230 Primer fo  
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M20011 Mus spretus  
BC004686 Mus muscu  
S43335 hprt-hypoxa  
X17656 C.longicaud  
BC000578 Homo sapi  
V00530 Human mRNA  
M31642 Human hypox  
J00060 Chinese ham  
L37778 Meriones un



**KEYWORDS** FLI\_CDNA.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
**REFERENCE** 1 (bases 1 to 807)  
**AUTHORS** Li, Y., Wu, T., Xu, S., Ren, S., Chen, Z. and Han, Z.  
**TITLE** A novel gene expressed in human liver cancer tissue  
**JOURNAL** Unpublished  
**REFERENCE** 2 (bases 1 to 807)  
**AUTHORS** Li, Y., Wu, T., Xu, S., Ren, S., Chen, Z. and Han, Z.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (19-JAN-2000) Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China  
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 /translation="MAGSEAPDYGRGVIMDDPXYDLNLFVPOHYGYDLEVLIPHGIIIVRERLAKIMKDIQYSDIMVLCLGKGYKCADLVHLKNIENSDFVSMKVDFIRKSTRNDQSGEMQIIGDDSLAGKRNVLIVEDVVGTRMKALLSIEKYKENIKVASLLVYKRSRSGDFRDPYAGFEIPNFVVGVALDYNFYRDLNHLICVINEHGKEKYRV"  
 BASE COUNT 239 a 157 c 205 g 206 t  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 9.13e-107 Length: 807  
 Score: 1065.00 Matches: 203  
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 Query Match: 95.43% Indels: 0  
 DB: 9 Gaps: 0  
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 Qy 27 HistTyrTyrGlyAspLeuGluTyrValLeuIleProHisGlyIleIleValAspArgIle 46  
 Db 117 CACTATTATGAGACTTGGAGTATGCTCATCCCTCATGGTATCATTTGGACAGAAATT 176  
 Qy 47 GluArgLeuAlaLysAspIleMetLysAspIleGlyTyrSerAspIleMetValLeuCys 66  
 Db 117 CACTATTATGAGACTTGGAGTATGCTCATCCCTCATGGTATCATTTGGACAGAAATT 176

177 GAGCGCGTGGCCAGGATATATGAAAGACATAGATATAGTGCATCATGCTGCTGTCT 236  
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RESULT 3  
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 LOCUS BC008662  
 DEFINITION Homo sapiens, HHGP protein, clone MGC:16888 IMAGE:3871911, mRNA, complete cds.  
 ACCESSION BC008662  
 VERSION BC008662.1 GI:14250449  
 KEYWORDS MGC.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1450)  
 AUTHORS Strausberg, R.  
 TITLE Direct Submission  
 JOURNAL Submitted (25-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
 REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov  
 COMMENT Contact: MGC help desk  
 Email: cgapps-remail.nih.gov  
 Tissue Procurement: ATCC

cdna Library Preparation: Life Technologies, Inc.  
 cdna Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
 DNA Sequencing by: Baylor College of Medicine Human Genome  
 Sequencing Center  
 Center code: BCM-HGSC  
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
 Contact: [villalon@bcm.tmc.edu](mailto:villalon@bcm.tmc.edu)  
 Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,  
 A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W.,  
 Muzny, D.M., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>  
 Series: IRAC Plate: 13 Row: k Column: 20  
 This clone was selected for full length sequencing because it  
 passed the following selection criteria: matched mRNA gi: 104333254.

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BASE COUNT 435 a 274 c 318 g 423 t

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 Best Local Similarity: 98.54% Mismatches: 2  
 Query Match: 95.43% Indels: 0  
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US-09-902-705-2 (1-212) x BC008662 (1-1450)

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Qy 47 GluArgLeuAlaLysAspIleMetLysAspIleGlyTyrSerAspIleMetValLeuCys 66  
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## RESULT 4

BD159230

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BD159230 1926 bp DNA linear PAT 17-JAN-2003  
 Primer for synthesizing full-length cDNA and use thereof.

BD159230

BD159230.1 GI:27864988

JP 2002191363-A/14073.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1926)

Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.,

Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.

Primer for synthesizing full-length cDNA and use thereof

Patent: JP 2002191363-A 14073 09-JUL-2002;

HELIX RESEARCH INSTITUTE

OS Homo sapiens (human)

PN JP 2002191363-A/14073

PD 09-JUL-2002

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AK021950			
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DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
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AUTHORS			
TITLE			
JOURNAL			
COMMENT			
FEATURES			
source			



Percent Similarity: 98.54% Conservatives: 1  
Best Local Similarity: 98.05% Mismatches: 2  
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US-09-902-705-2 (1-212) x BD146172 (1-783)  
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QY 67 ValLeuLysGlyGlyTyrLysPheCysAlaAspLeuValGluHisLeuLysAsnIleSer 86  
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LOCUS  
DEFINITION  
ACCESSION  
C. longicaudatus hprt mRNA for hypoxanthine (guanine)  
phosphoribosyltransferase.  
X59652

VERSION X59652.1 GI:461343  
KEYWORDS hprt gene; mutant.  
SOURCE Cricetulus longicaudatus (long-tailed hamster)  
ORGANISM Cricetulus longicaudatus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
Cricetulus.  
REFERENCE 1  
AUTHORS Wei, S.J., Chang, R.L., Bhachech, N., Cui, X.X., Merkler, K.A.,  
Wong, C.Q., Hennig, E., Yagi, H., Jerina, D.M. and Conney, A.H.  
TITLE Dose-dependent differences in the profile of mutations induced by  
(+)-7R,8S-dihydroxy-9S,10R-epoxy-7,8,9,10-tetrahydrobenzo(a)pyrene  
in the coding region of the hypoxanthine (guanine)  
phosphoribosyltransferase gene in Chinese hamster V-79 cells  
Cancer Res. 53 (14), 3294-3301 (1993)  
JOURNAL 93313862  
MEDLINE 8324741  
PUBMED 2 (bases 1 to 657)  
REFERENCE Wei, S.C.  
AUTHORS Direct Submission  
TITLE Submitted (08-FEB-1994) S.C. Wei, Rutgers The State University,  
College of Pharmacy, Laboratory for Cancer Research, Dept of  
JOURNAL Chemical Biology & Pharmacognosy, Piscataway NJ 08855, USA  
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US-09-902-705-2 (1-212) x CLHPRT (1-657)



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VERSION M20011.1 GI:194000  
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US-09-902-705-2 (1-212) x MUSHPTS (1-702)

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| | | | | | | | | | | | | | | | | | | | | | | | | | : :  
Db 121 GTGATTAAGCACAGACTGAAGACACTGCCGAGATCTCATGAAGAAGATGGAGGCCAT 180  
| | | | | | | | | | | | | | | | | | | | | | | | | | : :  
QY 61 AspIleMetValLeuCysValLeuleyglcylTyrlTyrlPheCysAlaAspLeuValclu 80  
| | | | | | | | | | | | | | | | | | | | | | | | | | : :  
Db 181 CACATTGTGCCCTCTGTGCTGTGAAGGGGGCTATAAATCTTTGCTGACTGCTGGAT 240  
| | | | | | | | | | | | | | | | | | | | | | | | | | : :  
QY 81 HisLeulyAsnIleSerArgSenSerAspArgPheValSerMetLysValAspPheile 100  
| | | | | | | | | | | | | | | | | | | | | | | | | | : :  
Db 241 TACATTAAAGCACTGAATAGAAATAGTCATAGATCCATCCCATGACTGTAGATTATTC 300  
| | | | | | | | | | | | | | | | | | | | | | | | | | : :  
QY 101 ArgLeulySerTyrArgAnaspGlnSerMetGlyCluMetGlnIlelledgtygly 120  
| | | | | | |

1 MetAlaThrArgSerProGlyValValIleMetAspTrpProGlyTyrAspLeuAsn 20  
QY

RESULT 9	
BC004686	
LOCUS	1281 bp mRNA linear ROD 16-APR-2003
DEFINITION	Mus musculus hypoxanthine guanine phosphoribosyl transferase, mRNA (cDNA clone MGC:6197 IMAGE:3500895), complete cds.
ACCESSION	BC004686
VERSION	BC004686.1 GI:13435620
KEYWORDS	MGC.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1281)
REFERENCE	
AUTHORS	Strausberg,R.L., Feingold,E.A., Grouse,L.H., Henchen,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Wagner,C.M., Schuler,G.D.,

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Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ILN1 at: http://image.llnl.gov
Series: IPAK Plate: 9 Row: e Column: 18
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 7305154.
Location/Qualifiers
1. .1281
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CZECH II"
/db_xref="taxon:10090"
/clone="MGC:6197 IMAGE:3500885"
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arose spontaneously from a senescent normal mammary

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(clonal) outgrowth infected with the virus MMV."

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/note="Vector: PCMV-SPORTc"
1. .1281
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62. .718
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BASE COUNT      380 a   230 c   272 g   399 t
ORIGIN
Alignment Scores:
Pred. No.:      1,27e-75      Length:      1281
Score:          782.00      Matches:      146
Percent Similarity: 81.49%      Conservative: 31
Best Local Similarity: 68.87%      Mismatches: 35
Query Match:      70.07%      Indels:      0
DB:              10      Gaps:      0
US-09-902-705-2 (1-212) x BC004686 (1-1281)
Qy 1 MetAlaThrArgSerProGlyValValIleMetAspTyrProGlyTyrAspLeuAsn 20
Db 62 ATGCGACCGCGAGTCCCGCGTGGTATAGCGATGATGACGAGTATGACCTAGAT 121
Qy 21 LeuPheThrTyrProGlnHisTyrTyrGlyAspLeuGluTyrValLeuIleProHisGly 40
Db 122 TTGTTTGTATACCTAATCATATATGCGGAGTATGCGAAAGTGTATTCTCTCATGGA 181
Qy 41 IleIleValAspArgIleGluArgLeuAlaLysAspIleMetLysAspIleGlyTyrSer 60
Db 182 CTGATTATGACAGGACTGAAGACTGCTCGAGATGTCATGACGAGATGGAGGCCAT 241
Qy 61 AspIleMetValLeuCysValLeuLysGlyGlyTyrLysPheCysAlaAspLeuValGlu 80
Db 242 CACATTGGCCCTCTGTGTCTCAGGGGGGCTATAAGTCTTGTGACCTGCTGGAT 301
Qy 81 HisLeuLysAsnIleSerArgAsnSerAspArgPheValSerMetLysValAspPheIle 100
Db 302 TACATTAAAGCAGCTAGATAGATAGTATAGATCCATCTCTAGCTAGATTTATC 361
Qy 101 ArgLeuLysSerTyrArgAsnAspGlnSerMetGlyCyluMetGlnIleIleGlyGly 120
Db 362 AGACTGAAGAGCTACTGTATATGATCAGTCAACCGGGGACATAAAGTATTGTGGAGAT 421
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Qy 121 AspLeuSerThrLeuAlaGlyLysAsnPheLeuIleValGluAspValValGlyThrGly 140
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Qy 141 ArgThrMetLysAlaLeuLeuSerAsnIleGluLysTyrLysProAsnMetIleLysVal 160
Db 482 AAAACAATGCAAACTTTGCTTTCCCTGTTAAGCAGTACAGCCCAAAATGTTAAGGTT 541
Qy 161 AlaSerLeuLeuValLysArgThrSerArgSerAspGlyPheArgProAspTyrAlaGly 180
Db 542 GCAAGCTTCTCTGTTGAAGAAGGACCTCTGAGAGTGTGGATACAGCCACAGACTTTTGTGGA 601
Qy 181 PheGluIleProHisLeuPheValValGlyTyrAlaLeuAspTyrAsnGluTyrPheArg 200
Db 602 TTTCGAATTCGACACAGAGTTGTTGTGATATGCCCTTGACTATATGAGTACTTCAGG 661
Qy 201 AspLeuAsnHisIleCysValIleAsnGluHisGly 212
Db 662 GATTTCGATCAGTTTGTGTCAATTAGTGAACACTGGA 697
RESULT 10
S43335
LOCUS      S43335      685 bp      mRNA      linear      PRI 08-MAY-1993
DEFINITION hprt=hypoxanthine phosphoribosyltransferase [cynomolgus monkeys,
ACCESSION  S43335
VERSION    S43335.1 GI:254239
KEYWORDS
SOURCE     Macaca fascicularis (crab-eating macaque)
ORGANISM   Macaca fascicularis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
            Cercopithecinae; Macaca.
REFERENCE  1 (bases 1 to 685)
AUTHORS   Harbach,P.R., Filipunas,A.L., Wang,Y. and Aaron,C.S.
TITLE     DNA sequence analysis of spontaneous and
            N-ethyl-N-nitrosourea-induced hprt mutations arising in vivo in
            cynomolgus monkey T-lymphocytes
JOURNAL   Environ. Mol. Mutagen. 20 (2), 96-105 (1992)
MEDLINE   92371466
PUBMED    1505533
REMARK    GenBank staff at the National Library of Medicine created this
            entry [NCBI Gibbsq 111886] from the original journal article.
FEATURES
            Location/Qualifiers
                source
                1..685
                /organism="Macaca fascicularis"
                /mol_type="mRNA"
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BASE COUNT 203 a 114 c 169 g 199 t  
ORIGIN

Alignment Scores:  
Pred. No.: 1.13e-75 Length: 685  
Score: 779.00 Matches: 145  
Percent Similarity: 83.02% Conservative: 31  
Best Local Similarity: 68.40% Mismatches: 36  
Query Watch: 69.80% Indels: 0  
DB: 9 Gaps: 0

US-09-902-705-2 (1-212) x S43335 (1-685)

Qy 1 MetAlaThrArgSerProGlyValValIleMetAspTyrProGlyTyrAspLeuAsn 20  
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Qy 21 LeuPheThrTyrProGlnHisTyrTyrGlyAspLeuGluTyrValLeulleProHisGly 40  
Db 67 TTATTCTGCATACCTAATCATTAATGCTGAGGATTTGGAAGGGTGTATTCTCTCATGCA 126  
Qy 41 IleIleValAspArgIleGluArgLeuAlaLysAlaMetLysAspIleGlyTyrSer 60  
Db 127 CTAATATGACGAGACTGAACGCTCTGCTGAGATGTGATGAAGAGAGATGGGAGCCAT 186  
Qy 61 AspIleMetValLeuCysValLeuLysGlyTyrLysPheCysAlaAspLeuValGlu 80  
Db 187 CACATGTAGCCCTCTGTGTCTGCTCAAGGGGGCTATTAATCTTGTCTGACCTGTGGAT 246  
Qy 81 HisLeuLysAsnIleSerArgAsnSerAspArgPheValSerMetLysValAspPheIle 100  
Db 247 TACATCAAGCACTGAATAGAAATAGTAGATGATGATGATGATGATGATGATGATGATGAT 306  
Qy 101 ArgLeuLysSerTyrArgAsnAspGlnSerMetGlyGluMetGlnIleIleGlyGly 120  
Db 307 AGACTGAAGAGCTATTGTATGATGACCACTGACAGGGGAGATGATGATGATGATGATGAT 366  
Qy 121 AspLeuSerThrLeuAlaGlyLysAsnPheLeuIleValGluAspValValGlyThrGly 140  
Db 367 GATCTCTCAACTTTAATCTGGAAGATGCTTGTGATGGAAGATATATATGACACTGGC 426  
Qy 141 ArgThrMetLysAlaLeuLeuSerAsnIleGluLysTyrLysProAsnMetIleLysVal 160  
Db 427 AARACGATCGACACTTGTCTTCTTCTGCTGAGGAGATATATCAAGATGCTCAGGTC 486  
Qy 161 AlaSerLeuLeuValLysArgThrSerArgSerAspGlyPheArgProAspTyrAlaGly 180  
Db 487 GCAAGCTTCTGTGTAAGAGCACTCCAGAGTGTGATGATGATGATGATGATGATGATGATGAT 546  
Qy 181 PheGluIleProHisLeuPheValValGlyTyrAlaLeuAspTyrAsnGluTyrPheArg 200  
Db 547 TTGAAATTCACAGCAAGTTTGTGTAGGATATGCTTGTGATGATGATGATGATGATGATGATGAT 606

Qy 201 AspLeuAsnHisIleCysValIleAsnGluHisGly 212  
Db 607 GATTGATCATCTTTGTGTCATAGTGAACCTGGA 642  
RESULT 11  
CLHPRTM  
LOCUS C.LONGICAUDATUS HPRT mRNA linear ROD 21-MAY-1992  
DEFINITION C.Longicaudatus HPRT mRNA for hypoxanthine guanine  
phosphoribosyltransferase.  
ACCESSION X17656  
VERSION X17656.1 GI:49514  
KEYWORDS hprt gene; hypoxanthine-guanine phosphoribosyltransferase; point  
mutation.  
SOURCE Cricetulus longicaudatus (long-tailed hamster)  
ORGANISM Cricetulus longicaudatus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
Cricetulus.  
REFERENCE 1  
AUTHORS Rossiter, F., Muzny, M., Caskey, T. and Fox, M.  
TITLE A Chinese hamster HPRT point mutation reverts to the wild-type  
sequence  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1222)  
AUTHORS Rossiter, F.  
TITLE Direct Submission  
JOURNAL Submitted (14-NOV-1989) Rossiter B. J. F., Institute for Molecular  
Genetics, Baylor College of Medicine, 1, Baylor Plaza, Houston,  
Texas 77030, USA  
COMMENT See also J00060.  
FEATURES  
Location/Qualifiers  
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/mol\_type="mRNA"  
/db\_xref="taxon:10030"  
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1..1222  
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17..673  
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ASLLVKRTSPSVGKPDFVGFGEIPDKFVGVYALDYNEVFRDLNHVCVISTGKAKYA  
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variation 420

[illegible]

RESULT 12  
BC000578

LOCUS	BC000578	1316 bp	mRNA	linear	PR1 12-JUN-2000
DEFINITION	Homo sapiens, hypoxanthine phosphoribosyltransferase 1 (lesch-Nyhan syndrome), clone MGC:1722 IMAGE:3163726, mRNA, complete cds.				
ACCESSION	BC000578				
VERSION	BC000578.1 GI:12653602				
KEYWORDS	MGC.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae. Homo

REFERENCE 1 (bases 1 to 1316)  
AUTHORS Strausberg R.  
TITLE *Isolation, characterization, and sequencing of the human*  
SOURCE *Journal of Molecular Biology*, 1986, 186, 1-13, 12 refs.

TITLE	Direct Submission	Submitted (15-NOV-2000)	National Institutes of Health, Mammalian
JOURNAL			

Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

REMARK USA NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT  
Contact: MGC help desk  
Email: cgapbs-remail.nih.gov

CDNA Library Preparation: Rubin Laboratory  
Tissue Procurement: ATCC  
CDNA Library: Dravens Inc. The T.M.A.C.B. Consortium (1991)

CDNA library arrayed by: the I.M.A.G.E. Consortium (JUNU)  
DNA Sequencing by: National Institutes of Health Intramural  
Sequencing Center (NISC)

Gaithersburg, Maryland;  
 Web site: <http://www.nisc.nih.gov/>

Contact: nisc\_mgc@nhgri.nih.gov  
Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,

Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins E., Legaspi, R.

Lim, M., Maduro, Q. L., Masiello, C., Mastrian, S. D., McCloskey, J. C., McDowell, J., Pearson, R., Snyder, B., Stantripop, S., Thomas, P. J.,

Tiongson, E. E., Touchman, J. W., Tsurgeon, C., Vogt, J. L., Walker, M. A., Zhang, L.-H. and Green, E. D.

Clone distribution: MGC clone distribution information can be found through the IMA C & Consortium/INM at: <http://image.llnl.gov>

Series: IRAL Plate: 5 Row: m Column: 19  
This clone was selected for full length sequencing because it  
through the 1.1 kb. Consolida/IRAL at: <http://image.llnwd.net>

FEATURES

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1. .1316
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/lab\_host="DH10B-R"  
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49..705  
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(Lesch-Nyhan syndrome)"  
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CDS

BASE COUNT 408 a 215 c 278 g 415 t  
ORIGIN

Alignment Scores:  
Pred. No.: 2,79e-75 Length: 1316  
Score: 779.00 Matches: 145  
Percent Similarity: 83.02% Conservative: 31  
Best Local Similarity: 68.40% Mismatches: 36  
Query Match: 69.80% Indels: 0  
DB: 9 Gaps: 0

US-09-902-705-2 (1-212) x BC000578 (1-1316)

QY 1 MetAlaThrArgSerProGlyValValIleMetAspTyrProGlyTyrAspLeuAsn 20  
|||||  
Db 49 ATGGCGACCGCAGCCTGGCGTCTGATTAGTATGATGATGAACGAGTTATGACCTTAT 108  
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QY 21 LeuPheThrTyrProGlnHisTyrTyrGlyAspLeuGluTyrValLeuIleProHisGly 40  
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Db 109 TTAATTGTCATACCTAATCATATTATGCTGAGGATTTCGAAGGGTGTATTCTCATGGA 168  
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QY 41 IleIleValAspArgIleGluArgLeuAlaLysAspIleMetLysAspIleGlyTyrSer 60  
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Db 169 CTAATTATGACGAGCTGAACCTCTGCTCGAGATGTCATGAAGGAGTGGAGGCCAT 228  
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QY 61 AspIleMetValLeuCysValLeuLysGlyTyrTyrLysPheCysAlaAspLeuValGlu 80  
|||||  
Db 229 CACATTGTAGCCCTCTGTGCTCTCAAGGGGGCTATAAAATCTTGTCTGACCTGTGGAT 288  
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QY 81 HisLeuLysAsnIleSerArgAsnSerAspArgPheValSerMetLysValAspPheIle 100  
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Db 289 TACATCAAGCACTGAATAGATAGTATGATCCATTCCTATGACTGTAGATTATTC 348  
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QY 101 ArgLeuLysSerTyrArgAsnAspGlnSerMetGlyGluMetGlnIleIleGlyGly 120  
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Db 349 AGACTGAAGAGCTATTGTAATACCACTGACACAGGGGACATAAAAGTAATTGTGGAGAT 408  
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QY 121 AspLeuSerThrLeuAlaGlyLysAsnPheLeuIleValGluAspValValGlyThrGly 140  
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Db 409 GATCTCTCAACTTTAACTGGAAGAAGATGCTTCTGATTGGAAGATATAATTGACACTGGC 468

QY 141 ArgThrMetLysAlaLeuLeuSerAsnIleGluLysTyrLysProAsnMetIleLysVal 160  
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Db 529 GCAAGCTTGTCTGTAAGAGGACCCACGAAGTGTGGATATAAGCCAGACTTTGTGGA 588  
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QY 181 PheGluIleProHisLeuPheValValGlyTyrAlaLeuAspTyrAsnGluTyrPheArg 200  
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Db 589 TTTGAAATTCACAGCAAGTTTGTGTAGGATATCCCTTGACTATAATGAATACCTTCAGG 648  
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QY 201 AspLeuAsnHisIleCysValIleAsnGluHisGly 212  
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Db 649 GATTGATCATGTTTGTGTGTCATTAGTGAAGACTGGA 684

RESULT 13

HSHPRT

LOCUS HSHPT 1331 bp mRNA linear PRI 02-JUL-1999  
DEFINITION Human mRNA encoding IMP:Pyrophosphate phosphoribosyltransferase  
E.C. 2.4.2.8.

ACCESSION V00530

VERSION V00530.1 GI:32449

KEYWORDS complementary DNA: transferase.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1331)

AUTHORS Jolly D.J., Okayama H., Berg P., Esty A.C., Filpula D., Bohlen P.,

Johnson G.G., Shively J.E., Hunkapillar T. and Friedmann T.

TITLE Isolation and characterization of a full-length expressible cDNA

JOURNAL for human hypoxanthine phosphoribosyl transferase

MEDLINE Proc. Natl. Acad. Sci. U.S.A. 80 (2), 477-481 (1983)

PUBMED 83169681

COMMENT 6300847

FEATURES Data kindly reviewed (30-MAY-1983) by D.J. Jolly.

source

Location/Qualifiers

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86..742

/note="coding sequence"

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BASE COUNT 385 a 237 c 281 g 428 t

ORIGIN

[illegible]

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QY	41	lIlelleValAspArgIleGluValLeuAlaLysAspIleMetLysAspIleGlyTyrSer	60
Db	206	CTAATTATGACGAGCACTGAACGTCCTGCTCGAGATGCTGATGACGAGATGGAGGCCAT	265
QY	61	AspIleMetValLeuCysValLeuLysGlyGlyTyrLysPheCysAlaAspLeuValGlu	80
Db	266	CACATTGTACCCCTCTGTGCTCAAGGGGGCTATAAATCTTTGCTGCACTGCTGGAT	325
QY	81	HisLeuLysAsnIleSerArgAsnSerAspArgPheValSerMetLysValAspPheIle	100
Db	326	TACATCAAGACACTGAATAGAAATAGTAGATCCATTCCTGACTGTAGATTATTC	385
QY	101	ArgLeuLysSerTyrArgAsnAspGlnSerMetGlyGluMetGlnIlelleGlyGlyGly	120
Db	386	AGACTGAGAGCATTGTGTATGACCACTGACAGGGACATAAAGTAATTTGTGGAGAT	445
QY	121	AspLeuSerThrLeuAlaGlyLysAsnPheLeulleValGluAspValValGlyThrGly	140
Db	446	GATCTCTCAACTTTAACTGGGAAGATGCTGTGTTGTGGAGATATAATTGCACCTGCG	505
QY	141	ArgThrMetLysAlaLeuLeuSerAsnIleGluLysTyrLysProAsnMetIleLysVal	160
Db	506	AAAAATCATGCAGACTTCTTCTTCTGCTGAGCAGCATATAATCCAAAGATGGTCAAGTC	565
QY	161	AlaSerLeuLeuValLysArgThrSerArgSerAspGlyPheArgProAspTyrAlaGly	180
Db	566	GCAGCTTGCTGCTGGAAAGACCCACAGAGTGTGGATATAAGCAGACTTTGTGTGA	625
QY	181	PheGluIleProHisLeuPheValValGlyTyrAlaLeuAspTyrAsnGluTyrPheArg	200
Db	626	TTTGAATTCGACACACTTGTGTGTAGATATGCCCTTGACTATATGATACTTCAGG	685
QY	201	AspLeuAsnHisIleCysValIleAsnGluHisGly	212
Db	686	GATTGATCATGTTTGTGCTATTAGTCAAACTGA	721
RESULT 15			
LOCUS	CRUHPRT		
DEFINITION	Chinese hamster hprt mRNA, complete cds.		
ACCESSION	J00060		
VERSION	J00060.1 GI:191112		
KEYWORDS	transferase.		
SOURCE	Cricetulus sp.		
ORGANISM	Cricetulus sp.		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;		
	Cricetulus.		
	1 (bases 1 to 1301)		
	Konecki,D.S., Brennand,J., Fuscoc,J.C., Caskey,C.T. and		
	Chinault,A.C.		
TITLE	Hypoxanthine-guanine phosphoribosyltransferase genes of mouse and		

**RESULT 15**

LOCUS	CRUHPRT	1301 bp	mRNA	linear	ROD 10-JUN-1993
DEFINITION	Chinese hamster hpvt mRNA, complete cds.				
ACCESSION	J00060				
VERSION	J00060.1 GI:191112				
KEYWORDS	transferase.				
SOURCE	Cricetulus sp.				
ORGANISM	Cricetulus sp.				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;				
	Cricetulus.				
REFERENCE	1 (bases 1 to 1301)				
AUTHORS	Konecki,D.S., Brenmand,J., Fuscoe,J.C., Caskey,C.T. and Chinsault,A.C.				
TITLE	Hypoxanthine-guanine phosphoribosyltransferase genes of mouse and				



Db 211 GTGATTATGGACAGGACTGAAAGACATTGCCCGAGATGTCTATGAAAGAGATGGAGGCCAT 270  
 QY 61 AspileMetValLeuCysValLeuLysGlyGlyTyrLysPheCysAlaAspLeuValGlu 80  
 Db 271 CACATTGTGGCCCTCTGTGCTGAGAGGGGGCTATAAATCTTGTGACCTGTGGAT 330  
 QY 81 HisLeuLysAsnIleSerArgAsnSerAspArgPheValSerMetLysValAspPheIle 100  
 Db 331 TACATTAAAGCAGCTGAATAGAAATAGTAGATCCATCCCATGACTGTAGATTTATC 390  
 QY 101 ArgLeuLysSerTyrArgAsnAspGlnSerMetGlyGluMetGlnIleIleGlyGly 120  
 Db 391 AGACTGAAGAGCTACTGTAAATGATCAGTCAACAGGGGACATAAAAGTTATTGTGGGAT 450  
 QY 121 AspLeuSerThrLeuAlaGlyLysAsnPheLeuIleValGluAspValValGlyThrGly 140  
 Db 451 GATCTCTCAACTTAACTGGAAGAGATGTTGATTTGTTGAGGACATAAATTGACACTGGT 510  
 QY 141 ArgThrMetLysAlaLeuLeuSerAsnIleGluLysTyrLysProAsnMetIleLysVal 160  
 Db 511 AAAACATGCAACTCTGCTTTCCCTGGTCAAGCGGTACACCTCAAAATGGTTAAGTT 570  
 QY 161 AlaSerLeuValLysArgThrSerArgSerAspGlyPheArgProAspTyrAlaGly 180  
 Db 571 GCAAGCTTGTGCTGAAAGGACCTCTCGAAGTGTTCATATAGCCAGACTTTGTTGA 630  
 QY 181 PheGluLeuProHisLeuPheValValGlyTyrAlaLeuAspTyrAsnGluTyrPheArg 200  
 Db 631 TTTCAAATTCACAGCAAGTTGTGTGTGATATGCCCTTGACTATATAGTACTCTCAGG 690  
 QY 201 AspLeuAsnHisIleCysValIleAsnGluHisGly 212  
 Db 691 GATTGATCATATTGTGTCTATTAGTCAAACTGGG 726

Search completed: October 4, 2003, 13:38:52  
 Job time : 2590 secs